

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|---------------------|
| 1 | 2.67 | 100.0 | 406 | 23 | AAU98047 | Human HGPBMY7 N-t |
| 2 | 2.67 | 100.0 | 406 | 23 | AAU98048 | Human HGPBMY7 C-t |
| 3 | 2.67 | 100.0 | 406 | 23 | AG361638 | Human G-protein-co |
| 4 | 2.67 | 100.0 | 406 | 23 | AAU10631 | Novel G-protein co |
| 5 | 2.67 | 100.0 | 419 | 22 | AAU08807 | Gallatin Receptor-1 |
| 6 | 2.67 | 100.0 | 419 | 22 | AA206761 | Human G-protein co |
| 7 | 2.67 | 100.0 | 419 | 22 | AG63344 | Amino acid sequenc |
| 8 | 2.67 | 100.0 | 419 | 22 | AAU04363 | Human G-protein co |
| 9 | 2.67 | 100.0 | 419 | 22 | AAU01848 | Human DNA G-protei |
| 10 | 2.67 | 100.0 | 419 | 22 | AA560691 | Human G-protein-co |

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|---------------------|
| 1 | 2.67 | 100.0 | 406 | 23 | AAU98047 | Human HGPBMY7 N-t |
| 2 | 2.67 | 100.0 | 406 | 23 | AAU98048 | Human HGPBMY7 C-t |
| 3 | 2.67 | 100.0 | 406 | 23 | AG361638 | Human G-protein-co |
| 4 | 2.67 | 100.0 | 406 | 23 | AAU10631 | Novel G-protein co |
| 5 | 2.67 | 100.0 | 419 | 22 | AAU08807 | Gallatin Receptor-1 |
| 6 | 2.67 | 100.0 | 419 | 22 | AA206761 | Human G-protein co |
| 7 | 2.67 | 100.0 | 419 | 22 | AG63344 | Amino acid sequenc |
| 8 | 2.67 | 100.0 | 419 | 22 | AAU04363 | Human G-protein co |
| 9 | 2.67 | 100.0 | 419 | 22 | AAU01848 | Human DNA G-protei |
| 10 | 2.67 | 100.0 | 419 | 22 | AA560691 | Human G-protein-co |

27-SEP-2000: 2000RS-235731P

CC polypeptide are useful for modulating intracellular calcium levels,
 CC modulating Ca²⁺ sensitive signalling pathways and modulating nuclear
 CC factor activator of transcription (NFAT) element associated signalling
 CC pathways. The present sequence is a representative sequence for a
 CC set of sequential C-terminal deletion mutants of HGRPMY7.

XX
 SQ Sequence 406 AA,
 Query Match 100.0%; Score 2167; DB 23; Length 406;
 Best Local Similarity 100.0%; Pred. No. 2.5e-191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNVSPALHFAAGYVLPDSQDWTIIIPALLVAVCLVGVNLCVIGILLHNAWKGPMSI 60
 DB 1 MNVSPALHFAAGYVLPDSQDWTIIIPALLVAVCLVGVNLCVIGILLHNAWKGPMSI 60
 QY 61 HCLILMLCEALCLLFLSAPIRATAYSKSVWDLGFWVCKSSDWFIIHTCMAKSLTIIVVA 120
 DB 61 HSLILNLSLADLSLLFLSAPIRATAYSKSVWDLGFWVCKSSDWFIIHTCMAKSLTIIVVA 120
 QY 121 KVCFMASDPAKQVSHNYTIWVSVVAITVAVSLLEPEWFFSTIRHHEGVENCLVDVPA 180
 DB 121 KVCFMASDPAKQVSHNYTIWVSVVAITVAVSLLEPEWFFSTIRHHEGVENCLVDVPA 180
 QY 191 VAEFMSMFKLPLAFGLPLFPASFYFWPAYDQCKPKGTQTNLPNQRISQVTVMLL 240
 DB 181 VAEFMSMFKLPLAFGLPLFPASFYFWPAYDQCKPKGTQTNLPNQRISQVTVMLL 240
 QY 241 SIATISALLWLPKVAWLWWHLKAAGPAPDQGFIALSQVLMFSISSANPLIFLVMSSEF 300
 DB 241 SIATISALLWLPKVAWLWWHLKAAGPAPDQGFIALSQVLMFSISSANPLIFLVMSSEF 300
 QY 301 REGLGKGVWMMITTKPPVSVESQETPAGNSEGLPKVPSPPSPASIPPEYVPSPPSGVG 360
 DB 301 REGLGKGVWMMITTKPPVSVESQETPAGNSEGLPKVPSPPSPASIPPEYVPSPPSGVG 360
 QY 361 KTEKAEIPLPQVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406
 DB 361 KTEKAEIPLPQVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406

RESULT 3
 ABG61638
 ID ABG61638 standard; Protein, 406 AA.

AC ABG61638;
 XX
 DT 13-AUG-2002 (first entry)
 DE
 DE Human G protein-coupled receptor HGRPMY7.

XX Human, G protein-coupled receptor, HGRPMY7, spinal chord,
 KW spinal chord-related disorder; breast cancer; neoplastic disease;
 KW brain disorder; leukaemia; myeloma; immunological disorder;
 KW cholecystitis; Grave's disease; osteoarthritis; asthma;
 KW neuropsychological disorder, dementia; depression; Alzheimer's disease,
 KW Down's syndrome; epilepsy; intracellular calcium level; NFAT;
 KW nuclear factor activator of transcription element.

OS Homo sapiens.
 XX
 XX WC000006923-A2.
 PN
 PD 04 APR 2002.
 XX
 XX 26-SEP-2001, 2001WO 030103;
 XX

PR 27-SEP 2000; 2000US-235731P.
 PR 14-FEB 2001; 2001US-268580P.
 PR 28 AUG 2001; 2001US-315423P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PI

PI Battaglino P, Feder JN, Mintier G, Ramanathan CS, Westphal R;

XX Hawken DR, Cacace A, Barber L, Kornacker MG;

DR WP1; 2002-435195/46.

DR N-PSDR; ABK84809.

XX

PT Novel human G-protein coupled receptor BMV7 (HGRPMY7) polypeptide,
 PT useful for modulators of HGRPMY7 activity that are useful for treating
 PT leukaemia, cholecystitis, Grave's disease, epilepsy, dementia,
 PT depression -

XX

PS Claim 11; Fig 2; 170pp; English.

XX The invention relates to an isolated polypeptide (i) comprising amino
 CC acid sequence that is at least 95% identical to a polypeptide fragment of
 CC a fully defined human G protein-coupled receptor BMV7 (HGRPMY7)
 CC polypeptide, or variant, allelic variant or species homologue.
 CC Also included are polynucleotides encoding the above polypeptides,
 CC expression vectors, host cells, anti-HGRPMY7 antibodies and modulators
 CC of HGRPMY7. HGRPMY7 and its polynucleotide are useful for diagnosis
 CC prevention, treating or ameliorating a medical condition e.g. a disease,
 CC disorder, or a condition related to brain, breast, gastrointestinal or
 CC musculo-skeletal systems, such that thalamus-, corpus callosum-,
 CC hippocampus-, caudate nucleus-, amygdala-, substantia nigra-,
 CC cerebellum-, brain-, breast-, colon-, spinal chord-related disorders,
 CC breast cancer, neoplastic diseases, and disorders related to spinal
 CC chord and brain. An antagonist or inhibitor of (i) identified using (i)
 CC is useful for treating a neoplastic disorder such as leukaemia, myeloma,
 CC immunological disorders such as cholecyctitis, Grave's disease,
 CC osteoarthritis, asthma, neurological disorders such as dementia,
 CC depression, Alzheimer's disease, Down's syndrome and epilepsy.
 CC HGRPMY7, its polynucleotide and agonists or antagonists of the
 CC polypeptide are useful for modulating intracellular calcium levels,
 CC modulating Ca²⁺ sensitive signalling pathways and modulating nuclear
 CC factor activator of transcription (NFAT) element associated signalling
 CC pathways. The present sequence is the HGRPMY7 protein sequence.

XX

SQ Sequence 406 AA;

Query Match 100.0%; Score 2167; DB 23; Length 406;

Best Local Similarity 100.0%; Pred. No. 2.5e-191;

Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSPALHFAAGYVLPDSQDWTIIIPALLVAVCLVGVNLCVIGILLHNAWKGPMSI 60

DB 1 MNVSPALHFAAGYVLPDSQDWTIIIPALLVAVCLVGVNLCVIGILLHNAWKGPMSI 60

QY 61 HSLILNLSLADLSLLFLSAPIRATAYSKSVWDLGFWVCKSSDWFIIHTCMAKSLTIIVVA 120

DB 61 HSLILNLSLADLSLLFLSAPIRATAYSKSVWDLGFWVCKSSDWFIIHTCMAKSLTIIVVA 120

QY 121 KVCFMASDPAKQVSHNYTIWVSVVAITVAVSLLEPEWFFSTIRHHEGVENCLVDVPA 180

DB 121 KVCFMASDPAKQVSHNYTIWVSVVAITVAVSLLEPEWFFSTIRHHEGVENCLVDVPA 180

QY 181 VAEFMSMFKLPLAFGLPLFPASFYFWPAYDQCKPKGTQTNLPNQRISQVTVMLL 240

DB 181 VAEFMSMFKLPLAFGLPLFPASFYFWPAYDQCKPKGTQTNLPNQRISQVTVMLL 240

QY 241 SIATISALLWLPKVAWLWWHLKAAGPAPDQGFIALSQVLMFSISSANPLIFLVMSSEF 300

DB 241 SIATISALLWLPKVAWLWWHLKAAGPAPDQGFIALSQVLMFSISSANPLIFLVMSSEF 300

QY 301 REGLGKGVWMMITTKPPVSVESQETPAGNSEGLPKVPSPPSPASIPPEYVPSPPSGVG 360

DB 301 REGLGKGVWMMITTKPPVSVESQETPAGNSEGLPKVPSPPSPASIPPEYVPSPPSGVG 360

QY 361 KTEKAEIPLPQVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406

DB 361 KTEKAEIPLPQVEQFWHERDTPVSVQDNDPIPWEHEDQETGEGVK 406

RESULT 4


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PF 15-MAP-2001; 2001WO-EP02925
XX
XX 16-MAP-2000; 2000US-0180994
PP 17-JUN-2000; 2000US-0210083
PR 07-DEC-2000; 2000US-0251515.
PA (FAPB) RAYER AG.
XX
XX Pamakrishnan S;
PI
XX
XX WPI; 2001-582449/65
DR N-PSDB; AAS13700.
XX
XX Reagent and methods of regulating a galanin receptor-like G protein
PT coupled receptors and their regulation for therapeutic purposes e.g.
PT treatment of hypertension and asthma -
XX
XX Claim 1; Fig 2; 123pp; English.
XX
XX The invention describes novel reagents and methods of regulating a
CC galanin receptor-like G-protein coupled receptor for therapeutic
CC purposes, useful for treating disease by gene therapy. A pharmaceutical
CC composition described in the specification is useful for modulating the
CC activity of the Galanin receptor-like GPCR in a pathophysiological
CC disorder, selected from obesity, diabetes, cardiovascular disease,
CC asthma, pain, depression, ischaemia, Alzheimer's disease, sleep disorder,
CC migraine, anxiety and reproductive disorder. Specifically, the
CC composition is useful for modulating the activity of the receptor in
CC cognition, analgesia, sensory processing, processing or visceral
CC information, motor coordination, modulation of dopaminergic activity and
CC neuroendocrine function. This sequence is the Galanin receptor-like
CC G protein coupled receptor described in the method of the invention.
XX
XX Sequence 419 AA;
SQ
Query Match 100.0%, Score 2167, EB 22; Length 419;
Best Local Similarity 100.0%; Pred No. 2 6e-191;
Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNVSPFHLHPAGGYLPSRSQDPTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPSMI 60
DB 14 MNVSPFHLHPAGGYLPSRSQDPTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGPSMI 73
QY 61 HSLILNLSLADIALLSFAPIPATAYSKSVMDLGMFVCKSSDWFHTCMAAKSLTIIVVVA 120
DB 74 HSLILNLSLADIALLSFAPIRATAYSKSVMDLGMFVCKSSDWFHTCMAAKSLTIIVVVA 133
QY 121 KVCFFVYASDPKQVSHNTYINSVLVAITVVASLLPLDPWFSTIRHHGVEMCLVDVPA 180
DB 134 KVCFFVYASDPKQVSHNTYINSVLVAITVVASLLPLDPWFSTIRHHGVEMCLVDVPA 193
QY 181 VAEERMSMFRTLYPILLAPLPIPFASFFYPWPAYDQCFKFGTKTQNLNWDIIRSKQVTVMLL 240
DB 194 VAEERMSMFRTLYPILLAPLPIPFASFFYPWPAYDQCFKFGTKTQNLNWDIIRSKQVTVMLL 253
QY 241 STAITALLLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLFLVWSEEF 300
DB 254 STAITALLLPEWVAWLWWHLKAAGPAPPQGFIALSQVLMFSSANPLFLVWSEEF 313
QY 301 PGLKGVNFWMTTKPTVTSQETPAGNSGLPKVPSPEPASIPKEKPSSSSGKG 360
DB 314 PGLKGVNFWMTTKPTVTSQETPAGNSGLPKVPSPEPASIPKEKPSSSSGKG 373
QY 361 KTEKAPILPDVQEQWHEHEDTVPSVQNDPIPWHEHEDQETGEGVK 406
DB 374 KTEKAPILPDVQEQWHEHEDTVPSVQNDPIPWHEHEDQETGEGVK 419
RESULT 6
ID AAE06761
XX AAE06761 standard; Protein, 419 AA
AC AAE06761;

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16-OCT-2001 (first entry)
Human G-protein coupled receptor-11 (GCRC-11) protein.

Human; G-protein coupled receptor-11; GCRC-11; cytostatic; hepatotropic; virucide; antiinflammatory; anticonvulsant; antiemetic; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilizer; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; psoriasis; cancer; neurological disorder; stroke; Alzheimer's disease; Huntington's disease; Parkinson's disease; cardiovascular disorder; epilepsy; hypertension; varicose vein; vasculitis; dysphagia; dyspepsia; anorexia; gastrointestinal disorder; pancreatitis; autoimmune disorder; Addison's disease; Crohn's disease; acquired immune deficiency syndrome; AIDS; uveitis; infection; trauma; metabolic disorder; diabetes; obesity; osteoporosis; transgenic animal; gene therapy.

Homo sapiens.

Key Location/Qualifiers
Domain 41..61 /label= Transmembrane_domain
Domain 53..133 /label= 7_transmembrane_receptor_domain
Domain 155..306 /label= 7_transmembrane_receptor_domain

WO2001:57085-A2.
09-AUG-2001.
01-FEB-2001; 2001WO-US03455.
02-FEB-2000; 2000US-0180093.
11-FEB-2000; 2000US-0182045.
(INCY-) INCYTE GENOMICS INC.
Baughn MR, Au Young J, Yue H,
WPI; 2001-488869/53.
N-PSDB; AAD12954.
Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic disorders -
Claim 1; Page 119-120; 138pp; English.
The present sequence is human G-protein coupled receptor-11 (GCRC-11) protein. The present invention relates to GCRC protein and nucleic acids encoding them. GCRC protein, its agonist or antagonist are useful for treating diseases or conditions associated with decreased expression or overexpression of functional GCRC in a patient, where the disorder is selected from cell proliferative disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzheimer's disease, Huntington's disease, Parkinson's disease, cardiovascular disorders such as hypertension, vasculitis, varicose veins, gastrointestinal disorders such as dysphagia, dyspepsia, anorexia, nausea, pancreatitis, autoimmune/inflammatory disorders such as acquired immunodeficiency syndrome (AIDS), Addison's disease, Crohn's disease, uveitis, viral, bacterial, fungal, parasitic, protozoal, helminthic infections, trauma and metabolic disorders such as diabetes, obesity, osteoporosis. GCRC proteins and their cDNAs are used to assess the effects of exogenous compounds on the expression of GCRC sequences. GCRC cDNA is useful to create knock in humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, for therapeutic or diagnostic purposes, for somatic or germline gene therapy, to generate hybridisation probes useful in mapping the naturally occurring genomic sequence, and in molecular biological

100

PR 23-DEC-1999; 99US-0171902.
 PR 11-FEB-2000; 2000US-0181749.
 PR 14-MAR-2000; 2000US-0189258.
 PR 14-MAR-2000; 2000US-0189258.
 PP 10-APR-2000; 2000US-0189259.
 PR 10-APR-2000; 2000US-0195899.
 PR 10-APR-2000; 2000US-0196078.
 PR 28-APR-2000; 2000US-0200419.
 PR 12-MAY-2000; 2000US-0201630.
 PR 12-JUN-2000; 2000US-0210741.
 PR 12-JUN-2000; 2000US-0210982.
 PR 21-AUG-2000; 2000US-0226760.
 PR 26-SEP-2000; 2000US-0235418.
 PR 26-SEP-2000; 2000US-0235779.
 PR 20-OCT-2000; 2000US-0242332.
 PR 20-OCT-2000; 2000US-0242343.
 XX (APEN-) APENA PHARM INC
 PA Chen R, Dang HT, Lowitz KP;
 PI WPI; 2001-355616/37.
 DR N-PSDB; AAS07936.
 XX Endogenous and non-endogenous versions of human G-protein coupled
 PT receptors for direct identification of candidate compounds as agonists,
 PT inverse agonists or partial agonists for use as therapeutic agents -
 XX Claim 5; Page 91-92; 160pp; English.
 PS The sequence represents a human G-protein coupled receptor (GPCR),
 CC hGPR9. The endogenous and non-endogenous, constitutively activated
 CC versions of human G-protein coupled receptors (GPCR), are useful for
 CC direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists having applicability as therapeutic
 CC agents for treating diseases related to GPCR, e.g. lung cancer.
 CC Non-endogenous version of human GPCRs are also utilized in research
 CC settings and in vitro and in vivo system, incorporating GPCRs can be
 CC utilised to elucidate and understand the roles these receptors
 CC play in the human condition, both normal and diseased.
 XX Sequence 419 AA;
 SQ Query Match 100.0%; Score 2167; DB 22; Length 419;
 Best Local Similarity 100.0%; Pred. No. 2.6e-191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
 QY 1 MNVSFAHLHPAGGYPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPMSI 60
 DB 14 MNVSFAHLHPAGGYPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPMSI 73
 QY 61 HSLILNLSLACLILLFSPAPIRATAYSKSVWDLGWFCVCKSSDWFHTCWAAKSLTIVVA 120
 DB 74 HSLILNLSLACLILLFSPAPIRATAYSKSVWDLGWFCVCKSSDWFHTCWAAKSLTIVVA 133
 QY 121 KVFEMVADSPAKQVSHNYITWSVLVAITWTVASLLPLPEWFFSTIRHIEGVEMCLVDVPA 180
 DB 134 KVFEMVADSPAKQVSHNYITWSVLVAITWTVASLLPLPEWFFSTIRHIEGVEMCLVDVPA 193
 QY 181 VAEEFMSMGKLYELLAFGLPLEFASFYFWRAYDOCKRGTKTONLRNQIRSKQVTVMLL 240
 DB 194 VAEEFMSMGKLYELLAFGLPLEFASFYFWRAYDOCKRGTKTONLRNQIRSKQVTVMLL 253
 QY 241 SIATISALLLPWVAVLWHLKAAGPAPPGQFIALSQVLMPFSISSANPLIFLWMSSEF 300
 DB 254 SIATISALLLPWVAVLWHLKAAGPAPPGQFIALSQVLMPFSISSANPLIFLWMSSEF 313
 QY 301 PEGLFKQVWMMITKPPVTVSESTETPAVNSSEGIPOKVPFSESPASIPKEKESPSGSGK 360
 DB 314 PEGLFKQVWMMITKPPVTVSESTETPAVNSSEGIPOKVPFSESPASIPKEKESPSGSGK 373
 QY 361 KTEKAEIPIIPDVEQFHWHERDTVPVSQDNDPIPWHEHEDQETGEGVK 406

Db 374 KTEKAEIPIIPDVEQFHWHERDTVPVSQDNDPIPWHEHEDQETGEGVK 419
 RESULT 9
 AAU01848
 ID AAU01848 standard; Protein; 419 AA.
 XX AAU01848;
 AC AAU01848;
 XX 07-SEP-2001 (first entry)
 DT Human DNA G-protein coupled receptor, PFI-001.
 XX Human; G-protein coupled receptor; PFI-001; mutant;
 KW chromosome 5; antibody; immunogen; signal transduction;
 KW obesity; diabetes; metabolic disease; neurological disease;
 KW psychotherapeutics; urogenital disease; reproduction; sexual medicine;
 KW inflammation; cancer; tissue repair; dermatology; skin pigmentation;
 KW photoregulation; frailty; osteoporosis; cardiovascular disease;
 KW gastrointestinal disease; anti-infection; allergy; respiratory disease;
 KW sensory organ disorder; sleep disorder; hair loss; melanin.
 XX Homo sapiens.
 OS EP1090989-A1.
 PN 11-APR-2001.
 PD 06-OCT-2000; 2000EP-0308851.
 PF 08-OCT-1999; 99GB-0023889.
 PR (PFI-001) PFI-001 LTD.
 PA (PFI-001) PFI-001 INC.
 XX Harland L;
 PI WPI; 2001-302045/32.
 DR N-PSDB; AAS03392.
 XX New human G-protein coupled receptor (GPCR) polynucleotide and
 PT polypeptide, useful in drug screening, as well as diagnosing of
 PT treating diseases associated with signal transduction, e.g. obesity,
 PT inflammation, tissue repair or cancer -
 XX Claim 22; Page 19; 46pp; English
 PS The sequence represents PFI-001, a Human G-protein coupled receptor.
 CC The gene encoding PFI-001 is located on human chromosome 5.
 CC Antibodies against PFI-001 and compounds which modulate its
 CC activity are useful as pharmaceuticals, for manufacturing a
 CC medicament for treating a patient having a need to modulate (i.e.
 CC (selectively) antagonise or agonise) PFI-001, and for evaluating and/or
 CC screening agents that can modulate PFI-001. The nucleic acid is also
 CC useful in gene therapy. The nucleic acid and encoded protein are useful
 CC for screening drug candidates for treating diseases associated with
 CC signal transduction such as obesity, diabetes and metabolic disease,
 CC neurological disease, psychotherapeutics, urogenital disease, sexual
 CC reproduction and sexual medicine, inflammation, cancer, tissue repair,
 CC dermatology, skin pigmentation, photoregulation, frailty, osteoporosis,
 CC cardiovascular disease, gastrointestinal disease, anti-infection,
 CC allergy and respiratory disease, sensory organ disorders, sleep disorders
 CC or hair loss.
 XX Sequence 419 AA;
 SQ Query Match 100.0%; Score 2167; DB 22; Length 419;
 Best Local Similarity 100.0%; Pred. No. 2.6e-191;
 Matches 406; Conservative 0; Mismatches 0; Indels 0; Gaps 0,
 QY 1 MNVSFAHLHPAGGYPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPMSI 60
 DB 14 MNVSFAHLHPAGGYPDSQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPMSI 73

Best Local Similarity 99.8%; Pred. No. 4.8e-191;
Matches 405; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSPFAHLRFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAWKPKSMI 60
DB 14 MNVSPFAHLRFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAWKPKSMI 73

QY 61 HSLILNLSLADLSLLFSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 120
DB 74 HSLILNLSLADLSLLFSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 133

QY 121 KVCFMVASTPAKQVSHNYTIVMSVLVAITVASLLFLPEWFFSTIRHHEGVEMCLVDVPA 180
DB 134 KVCFMVASTPAKQVSHNYTIVMSVLVAITVASLLFLPEWFFSTIRHHEGVEMCLVDVPA 193

QY 181 VAEEFMSMFPIYLLAFGLPLFPASFPYFPAVQCKYKPTQNLNRCQIRSKQVTVMLL 240
DB 194 VAEEFMSMFPIYLLAFGLPLFPASFPYFPAVQCKYKPTQNLNRCQIRSKQVTVMLL 253

QY 241 STAIISALLMLPEWVAVLWVHLKAAGPAPPGQFIALSQVLMFSSISANPLIFLVMSEEF 300
DB 254 STAIISALLMLPEWVAVLWVHLKAAGPAPPGQFIALSQVLMFSSISANPLIFLVMSEEF 313

QY 301 REGLGKGVWVWMTYKPTVSESQETPAGNSGGLPDKVPSPSPASIPPEKPSPPSSGKG 360
DB 314 REGLGKGVWVWMTYKPTVSESQETPAGNSGGLPDKVPSPSPASIPPEKPSPPSSGKG 373

QY 361 KTERAEIPIIPDVEQFWHERDTVPSCVDNDPIPWEHEDQETGEGVK 406
DB 374 KTERAEIPIIPDVEQFWHERDTVPSCVDNDPIPWEHEDQETGEGVK 419

RESULT 14
AAG64120
ID AAG64120 standard; Protein; 419 AA.
XX AAG64120;
DT 25-SEP-2001 (first entry)
DE Human 3 protein-coupled receptor GPRV16.
XX Human; guanosine triphosphate binding protein-coupled receptor;
KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;
KW Alzheimer's disease; cytostatic; hepatotropic; neurotropic;
KW neuroprotective; gene therapy; peptide therapy.
XX Homo sapiens.
XX WO200148188-A1.
XX 05-JUL-2001
XX 28-DEC-2000; 2000WQ-JF0409.
XX 28-DEC-1999; 09JP 0375152
PR 31-MAR-2000; 2000JP 010339.
XX (HELI-) HELIX RFS INST.
XX Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;
XX WPI; 2001-425662/45.
DR N-PSDB; AAH73533.
XX New DNA encoding guanosine triphosphate binding protein coupled
PT receptors and their expression products for screening potential
PT anticancer and neurotropic drugs and in diagnosis of these diseases
XX
PS Example 1: Page 108-111; 170pp; Japanese.
XX

CC The invention relates to nine human guanosine triphosphate binding
CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,
CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the
CC genes encoding them. These genes and proteins and antibodies against
CC the protein are useful in the treatment, prevention, diagnosis and
CC investigation of diseases associated with G protein-coupled receptors,
CC including cancer, cirrhosis of the liver and Alzheimer's disease.
CC The present sequence is a G protein coupled receptor of the invention.

XX Sequence 419 AA;
SQ

Query Match 99.3%, Score 2164, DB 22; Length 419;
Best Local Similarity 99.8%; Pred. No. 4.8e-191;
Matches 405; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSPFAHLRFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAWKPKSMI 60
DB 14 MNVSPFAHLRFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAAWKPKSMI 73

QY 61 HSLILNLSLADLSLLFSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 120
DB 74 HSLILNLSLADLSLLFSAPIRATAYSKSVMDLGFVCKSSDWFHTCMAAKSLTIIVVA 133

QY 121 KVCFMVASTPAKQVSHNYTIVMSVLVAITVASLLFLPEWFFSTIRHHEGVEMCLVDVPA 180
DB 134 KVCFMVASTPAKQVSHNYTIVMSVLVAITVASLLFLPEWFFSTIRHHEGVEMCLVDVPA 193

QY 181 VAEEFMSMFPIYLLAFGLPLFPASFPYFPAVQCKYKPTQNLNRCQIRSKQVTVMLL 240
DB 194 VAEEFMSMFPIYLLAFGLPLFPASFPYFPAVQCKYKPTQNLNRCQIRSKQVTVMLL 253

QY 241 STAIISALLMLPEWVAVLWVHLKAAGPAPPGQFIALSQVLMFSSISANPLIFLVMSEEF 300
DB 254 STAIISALLMLPEWVAVLWVHLKAAGPAPPGQFIALSQVLMFSSISANPLIFLVMSEEF 313

QY 301 REGLGKGVWVWMTYKPTVSESQETPAGNSGGLPDKVPSPSPASIPPEKPSPPSSGKG 360
DB 314 REGLGKGVWVWMTYKPTVSESQETPAGNSGGLPDKVPSPSPASIPPEKPSPPSSGKG 373

QY 361 KTERAEIPIIPDVEQFWHERDTVPSCVDNDPIPWEHEDQETGEGVK 406
DB 374 KTERAEIPIIPDVEQFWHERDTVPSCVDNDPIPWEHEDQETGEGVK 419

RESULT 15
AAU73244
ID AAU73244 standard; Protein; 418 AA.
XX AAU73244;
AC AAU73244;
DT 12-MAR-2002 (first entry)
DE Human potential G protein-coupled receptor.
XX Human; G protein-coupled receptor; GPCR; GALT4, galanin receptor;
KW Alzheimer's disease; amyotrophic lateral sclerosis; asthma;
KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiovascular;
KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;
KW depression; epilepsy; macular degeneration; lymphoma; melanoma;
KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;
KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;
KW tuberculosis; cognition disorder; memory disorder; anorexia;
KW hormonal release disorder; cardiovascular activity disorder;
KW pain perception disorder; obesity; diabetes; diabetes; obesity;
KW diabetes; hyperlipidaemia; stroke; gene therapy.
XX Homo sapiens.
OS
XX WO200185791-A1.
PN
PD 15-NOV-2001.
XX
XX 11-MAY-2001; 2001WO-US15332.

XX 11-MAY-2000: 2000US.203217P.
PR 19-MAY-2000: 2000US.203245P.
XX (LIFE-) LIFESPAN BIOGRAPHIES INC
PA Brown JP, Miller M, Burmer G, Fabre-Suver C, Pritchard D;
XX WPI: 2002-064505/09
PR N-PSOP: AAS90058, AAS90104
XX Novel G protein-coupled receptor polypeptides including galanin
PT receptor polypeptides useful for identifying modulators that are useful
PT for treating Alzheimer's disease, psoriasis, melanoma, multiple
PT sclerosis, stroke
XX

PS Disclosure: Page 122, 144pp; English.

XX The invention relates to an isolated polypeptide encoded by a
CC nucleic acid molecule that is at least 80% identical to the G
CC protein-coupled (GPCR) polynucleotides included in the specification.
CC Also included are probes based on the GPCR sequences (including
CC antisense probes), a host cell comprising an expression vector comprising
CC the GPCR sequence, antibodies raised against the polypeptides,
CC and methods of identifying modulators of the polypeptides. The
CC polypeptides are useful for identifying modulator compounds which
CC function as modulators, activators, repressors, agonists or antagonists
CC of the novel GPCR polypeptides including the GAL4 polypeptide. The
CC antibodies and nucleic acid probes as described above can be used to
CC detect the presence of the polypeptides and nucleic acids and are used to
CC diagnose a variety of diseases or disorders in which GPCRs are involved
CC e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma,
CC atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy,
CC chondrosarcoma, chronic obstructive pulmonary disease, Crohn's disease,
CC depression, epilepsy, macular degeneration, lymphoma, melanoma,
CC multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease,
CC psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis,
CC tuberculosis and many other diseases listed in the specification. The
CC probes and antibodies are also useful for diagnosing cognition and memory
CC disorders, anorexia, hormonal release disorders, cardiovascular activity
CC disorders, pain perception disorders, obesity, diabetes, Alzheimer's
CC disease. Preferably, compounds that decrease or increase
CC the expression of galanin receptor (GAL4) can be used to treat obesity,
CC diabetes, hyperlipidaemia and stroke. The GPCR nucleic acid is
CC useful for treating the above mentioned disorders by gene therapy
CC techniques. The present sequence is a novel GPCR of the invention.

XX Sequence 418 AA;

Query Match 99.8%; Score 2162, DB 23, Length 419,
Best Local Similarity 100.0%; Pred. No. 7 4a-191;
Matches 405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNVSFAHLHFAGGYIPSTSQDWFTIIPALLVAVCLVGVFVGNLCVIGILLINAWKGPMSI 60
DB 14 MNVSFAHLHFAGGYIPSTSQDWFTIIPALLVAVCLVGVFVGNLCVIGILLINAWKGPMSI 73
QY 61 HSLILNLSADLSLLFSPAPIATATYSKVDWLGWFCVYSSDWFTHTCMAAFSLTIIVVA 120
DB 74 HSLILNLSADLSLLFSPAPIATATYSKVDWLGWFCVCKSSDWFIHTCMAAKSLTIIVVA 133
QY 121 KYTEMVASIGAPQVSTHNYTIWSVLVAIWTVASLLPLPEWFFSTIPRHHEGVEMCLVDVPA 180
DB 134 KYCFMYASDPKQVSTHNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPA 193
QY 191 VAFEMSMGCKLYPLAFCLPLFPFASFEWPRAYDOGYPCYCTONTNPIQYISKYQVTUML 240
DB 194 VAEEMSMGCKLYPLAFCLPLFPFASFEWPRAYDOGYPCYCTONTNPIQYISKYQVTUML 253
QY 241 SIATISALLWLPFWVAVLWVWHLKAGAPPOCFIALSQVLMFSSISSANPLIFLWMSSEF 300
DB 254 SIATISALLWLPFWVAVLWVWHLKAGAPPOCFIALSQVLMFSSISSANPLIFLWMSSEF 313

Search completed: January 28, 2003, 11:50:26
Job time : 41 secs

QY 181 VAEFSSMFKLYDI LAFGLPEFASFWPAVDQCKKCKTKTQNLNPOIRSKQVTVMLL 240
 Db 194 VAEFSSMFKLYDI LAFGLPEFASFWPAVDQCKKCKTKTQNLNPOIRSKQVTVMLL 253
 QY 241 SIAIISALLLPEWVAWLWWHLKAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEF 300
 Db 254 SIAIISALLLPEWVAWLWWHLKAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEF 313
 QY 301 PFCLEKVVWMMITFKPPTVSQETPAGNSGLPRVVPSPSPASIPFVYSSSSSGHG 360
 Db 314 PFCLEKVVWMMITFKPPTVSQETPAGNSGLPRVVPSPSPASIPFVYSSSSSGHG 373
 QY 361 FTEFAFIPPI PVVEQFWHEDPTVSVQNDPDPWEHEDQFTGEGV 406
 Db 374 FTEFAFIPPI PVVEQFWHEDPTVSVQNDPDPWEHEDQFTGEGV 416

RESULT 2

ID Q9NEV1 PRELIMINARY; PRT; 380 AA.
 AC Q9NEV1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE G-protein coupled receptor
 GN ORPH 3.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 CC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N A.
 RA Saunders S.F., Burke J.F., Benjamin P.R.;
 PT "Multimeric CREB binding sites in the promoter regions of a family of
 FT alpha 5 protein-coupled receptors related to the vertebrate galanin
 RL and nociceptin/orphanin-FQ receptor families";
 RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AJ270461; C267264.1;
 DR HSSP: P02660; IPR4
 IF InterPro: IPR000017; GPCR_FH-1psn
 DR Pfam: PF000017; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PR01570; NPFFRECEPTOR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
 DR PROSITE: PS02622; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane
 CQ SEQUENCE 380 AA, 43664 MW, 40246 Da, pI=4.26

Query Match 11.6%; Score 251; DB 5; Length 380;
 Best Local Similarity 53.2%; Pred. No. 4.2e 13;
 Matches 89; Conservative 68; Mismatches 153; Indels 74; Gaps 13.

QY 11 AGGY-----LPDS-----QDW-----RTIIPALLVAVCLVGFV 39
 Db 3 AGLADAHINLRSQSVSTIYPTNTAAAHNESNMGEFYVVIIVTFPGVIGLGF 62
 QY 40 GNLGVGILLHNWAKGPMHSLNLSLADLSLLSPAPATAYSQVMDLQWVCK 99
 Db 63 GNLGVVTVVSD--KMPNTNTIILIPAVADLFLPCVPTATGALPVWPFSDIGCF 120
 QY 100 GSEWFTHINAAKELTIIVVAVYVGFVVASIPAKVGVIIH-VTIWSVLVAITVA-----SL 154
 Db 121 MTQYAMVVCAYAVYTIIVMSLDPLVAVVHAIPSMILPSEPTNPAILIITIIICGNT 180
 QY 155 IPIPPFPFSTIRHGVEMCL-----VTVAVABEENS-----MFGKLYPL-----LAFGLPEF 203
 Db 181 ILQGFVFNVTVEGRNPASCLNLKELFEAGAFPSSELFEGYVIFLGVITMLMYGLMY 240
 QY 204 PASFVYFWPAVQCKFKTKTQNLNPLNPLPSPQVTVMLLSIAISALLLPEWVAWLWWHL 263
 Db 241 PILYGV-----VPTGQNSRESIPAYPPVTPMVIVVVISAILCWLPIQILFAEPFG 292

QY 264 KAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEFEEGHLKVV 413
 Db 293 HAPITFHTSTFMAAGCLAYMGCVPILYAFLENEFFFEFLSTFTEWFFVWV 436
 QY 312 ----ITKKPPTVSQETPAGNSE 331
 Db 353 VPFTVTEK-PTTTTQCTGVNSK 376

RESULT 3

ID Q9NEV2 PRELIMINARY; PRT; 380 AA.
 AC Q9NEV2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE G-protein coupled receptor
 GN ORPH 2.
 OS Lymnaea stagnalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 CC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N A.
 RA Saunders S.F., Burke J.F., Benjamin P.R.;
 PT "Multimeric CREB binding sites in the promoter regions of a family of
 FT alpha 5 protein-coupled receptors related to the vertebrate galanin
 RL and nociceptin/orphanin-FQ receptor families";
 RT Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL: AJ270460; C267263.1;
 DR HSSP: P02660; IPR4
 IF InterPro: IPR000017; GPCR_FH-1psn
 DR Pfam: PF000017; 7tm1.1;
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PR01570; NPFFRECEPTOR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
 DR PROSITE: PS02622; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane
 CQ SEQUENCE 380 AA, 43664 MW, 40246 Da, pI=4.26

Query Match 11.4%; Score 247.5; DB 5; Length 380;
 Best Local Similarity 22.7%; Pred. No. 7.9e 12;
 Matches 79; Conservative 68; Mismatches 144; Indels 69; Gaps 13.

QY 23 FTIIPALLVAVTVTVFVQNLGVITLILHNWYPTQVMDLQWVCK 99
 Db 46 PIIVTFPGVICTLGLSGNSIVIPWVSD--KMPNTNTIILIPAVADLFLPCVPTATGALPVWPFSDIGCF 120
 QY 83 ATAYSKSWELNWFVYVSSQWTFHFWAARFLLVTVVAPFLWYASIFAPLVNHN 134
 Db 104 ATGVALPWPGRGIGTPTGVAVYVAVAYSVTVIVSSGRTAVVGRVDMVGRNT 164
 QY 142 WSVLVAVATVA--SILTFEFEECTIRHGFVEMT 199
 Db 164 WFAILLIILIGNTPIILGFGVFNVHGENRSALNLKIFELKELKAFVSEF 214
 QY 191 KLYPL-----LAFGLPEFAPFVFAVQVYFF 240
 Db 224 YVIFLGVITMLMYGLM-----KPLIYGVWVDFVNSAGSTAKPPTVWV 263
 QY 240 LSTAIISALLLPEWVAWLWWHLKAAGPAPQGFIALSQVLMFSISSANPLIFLVMSEEF 300
 Db 269 VIVVVFACWLPIQIILFAERFGHAPNTIPHISTGSAANVLAAMNVDNPLVABLSH 331
 QY 300 PFCLEKVVW-----FWTAKFTVSSQRTASNE 360
 Db 329 PPSRPFVLOCSTESSRMEVNTVPTVTP 429

RESULT 4

Q23497
ID Q23497 PRELIMINARY; PRT; 444 AA.
AC Q23497;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 24455 3 protein
GN ZK455.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
PL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=98069611; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology.";
RL Science 280, 2012-2018 (1998).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; Z66567; CAA91489.1;
DR InterPro; Ipp000276; GPCP_Phodfsn
DR Pfam; PF00001; 7tm 1; 1.
DR PROSITE; PS00237; G-PROTEIN RECP F1.1; 1.
DR PROSITE; PS00242; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
SQ SEQUENCE 444 AA; 498.4 MW; 2CF4F429B302A2 CRC64;

Query Match 10.9%; Score 236; DS 5; Length 444;
Best Local Similarity 24.8%; Pred. No. 7.9e-11;
Matches 84; Conservative 60; Mismatches 127; Indels 68; Gaps 12;

QY 25 IIPALLVAVCLVGFVGNLCVIGILLHNAWKGFQGMHSLILNLSLADLSLLPSAPTR 84
DB 45 IIPTFVAVILVGLVGNALVAVRQMR---NSTNTLITGLAISLDMFLLCVPTAV 101
QY 85 AYKSKVMDLGFVCKSSDMFIHTCMAKSLTIIVVAVKCFMVYADPAKQVSI---HNYTI 141
DB 102 DYAAPTWIPREWTCSMNFQHTSAVCSVWTLTLMALDYLAVVYVESMTLRPTNTVI 161
QY 142 MSVLVAIWTVASLLPLUPFFSTIRHH-----EGVEMCLVDVPAVAEE----- 184
DB 162 ALGFIIVITIASQIPVG-----FMHGIVYVDYFIMEKREKSTCAITLTATATPTMARTY 214
QY 185 FM---SMFGKLYPLAFGLPLFASFFWPAVDQCYKPGTKT---QNLRNQ-----IR--- 231
DB 215 FNTFVFVYVPL EISVLVGLMLPYLWMPFCISQSVGCRNLTNFGSGSTIPPP 271
QY 232 -----SKQVTMLSLAISALMLPEWVAVLWVHLKAGAPAPQGGFI----- 275
DB 272 EATAAKPKVTPVLVCLITWALCMLNVCFF ---MSGLAYPEPLVISHGVIMVIVQ 325
QY 276 ALSQVLMFSISSANPLIFLWMSPEEGLKGYWYWMITK 314
DB 326 IASQVLAITTECLNPLIYALMSQSPFEPVPMKLINK 364

RESULT 5
Q9NFV0
ID Q9NFV0 PRELIMINARY; PRT; 380 AA.
AC Q9NFV0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE G-protein coupled receptor.
GN ORPH 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Fulmonata; Bascommatophora;

Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RN [1]
RP SEQUENCE FROM N.A.
RA Saunders S.E., Burke J.F., Benjamin P.R.;
RT "Multimeric CREB binding sites in the promoter regions of a family of
orphan G-protein coupled receptors related to the vertebrate galanin
RT and nociceptin/orphanin-FQ receptor families";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AJ270462; CAB77265.1;
DR HSP; P02699; IBOJ
DR InterPro; Ipp000276; GPCP_Phodfsn
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PF00237; GPCPPHODPSN
DR PRINTS; PR01570; NFFRECEPTOR.
DR PROSITE; PS00247; G-PROTEIN RECP F1.1; 1.
DR PROSITE; PS00242; G-PROTEIN RECP F1.2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 380 AA; 42723 MW; D54F5B29B9E4C4 CP664;

Query Match 10.7%; Score 232.5; DS 5; Length 380;
Best Local Similarity 22.6%; Pred. No. 1.7e-10;
Matches 79; Conservative 69; Mismatches 142; Indels 57; Gaps 11;

QY 23 RTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGFQGMHSLILNLSLADLSLLPSAPTR 82
DB 46 RIIVTFGVICILGLFNSLILVIVSD---KIMRNTNLTLLSLAVADLFLPCVPT 103
QY 83 ATAYSKVMDLGFVCKSSDMFIHTCMAKSLTIIVVAVKCFMVYADPAKQVSI---HNYTI 141
DB 104 ATGYALPWPFGDGGKQVQVAVYVTVIVMSLDYLVAVVHAKSMILKSRNT 163
QY 142 MSVLVAIWTVASLLPLUPFFSTIRHH-----EGVEMCLVDVPAVAEE-----FMS- 189
DB 164 WFAIILIIIIILCGNTFLLQGFVNVVHGENRSACL NLKELKEHGAFAFGSLFF 222
QY 190 GKLYPL---LAFGLPLFFASFFWPAVDQCFPR-----STFTMLENLTISKAVTM 238
DB 223 GVIPLGVTVMLYGLML-----KRLLVGVVIGVGNQAGESIAKREATEM 267
QY 239 LLSIAIISALMLPEWVAVLWVHLKAGAPAPQGGFIALSQVLMFSISSANPLIFLWASE 298
DB 268 VVIVVIFALCMLPIQLIFAEFGHAPNTLHSTMAACCAAYMCCVNFILWFLSL 327
QY 299 EREGSLGWV---KMMITKFTVTSFQPTACNSE 331
DB 328 NPRESFRLQCTESSRMEYERINVTVEIK-ETIILKQCTWNSK 375

RESULT 6
Q9W6I3
ID Q9W6I3 PRELIMINARY; PRT; 411 AA.
AC Q9W6I3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Substance P receptor.
GN ASPR
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Sia G.M., Maggio J.E., Too H.P.;
RT "Construction of a functional EGFP-tagged avian substance P
RT receptor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)

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CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
DR EMBL: AF131057; AAF31017.1;
DR HSP; P29274; IMMH.
DR InterPro: IPR000276; GPCR_Phosph.
DR Pfam: PF00001; 7tm 1; 1
DR PRINTS: PS00237; GPCRPHOSPN.
DR PRINTS: PR01565; NEUROMEDINUR.
DR PRINTS: PR01570; NPPRRECEPT.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 411 AA; 47090 MW; 4584862A44150 CPO64.

Query Match
Best Local Similarity 24.1%; Pred No 2 10;
Matches 90; Conservative 50; Mismatches 142; Indels 57; Gaps 12.

CY 22 WPTIIFALLVA-VLVGFVSNVWVIGIILHNAMKFSFMSHLSLNLADLSLLFSAP 80
DB 116 VNFVALGESEVFTARTTFEINFEETAVTAGVYNTAAATPMAATPDKRATAT 176
CY 140 TMSVVAIVAVASLLPELPEFESTIPHHGVMTLVAVAHKMS MPRLY 104
DB 136 FIVISINWLAFAAFVLYFPPMPFSTTLYNTFGLTGTGTTGTTGTTGTTGTT 176
CY 134 PLLAPFLPLFPAPVPRAY GQPFKIPYKLEKELKELKELKELKELKELKELK 140
DB 134 PLLMATTIVVJHNSSEH RQTF VLFAPAPAPAPAPAPAPAPAPAPAPAPAP 140
CY 250 WLEPWV... - - - - - AAWTWHLFAAATATPTPTPTPTPTPTPTPTPTPTPT 150
DB 247 WLEPHVETATVGLNRPVY - - - - - LQVIA - - - - - WNTVWNTVWNTV 150
CY 238 FEREGLPQYMPW 310
DB 336 KPPAPGPPAPPW 348

RESULT 8
Q9JKN0 PRELIMINARY, PRT, 452 AA.
AC Q9JKN0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurokinin-3 receptor.
GN TACR3
OS Mus musculus (Mouse).
OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
PN [1]
PP SEQUENCE FROM N A
RC TISSUE=BRAIN.
RA Peled J.A., Brun K.A.;
RT "Molecular cloning and characterization of the murine neurokinin-3
RT receptor."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ database.
CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF233341; AAF62517.1;
DR HSP; F02699; IP88.
DR M01, M01; A02464; Tacr3.
DR InterPro: IPR000276; GPCR_Phosph.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PS00237; GPCRPHOSPN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 452 AA; 51026 MW; 7A46D400AD7FC44 CPO64.

Query Match
Best Local Similarity 23.9%; Pred No 3 10;
Matches 90; Conservative 63; Mismatches 161; Indels 67; Gaps 10.

CY 22 WPTIIFALLVA-VLVGFVSNVWVIGIILHNAMKFSFMSHLSLNLADLSLLFSAP 80
DB 70 WFIALWSLAVLVAVAVFQNIYVWII AHPVETVTVNYFVLAATAFASMSAFITV 91
CY 81 IPATAYSFQWGLCWVGYSSWFIHTCWAASLTIVVAVVCFVYASDPQVSHNYT 140
DB 128 VNFYVHCEVYDARVCKRQTFETAVTAGVYNTAAATPMAATPDKRATAT 176
CY 140 TMSVVAIVAVASLLPELPEFESTIPHHGVMTLVAVAHKMS MPRLY 104
DB 198 YI-VIGSIWILAEIAPP-ETISFIVMGLDLYVWGLDLYVWGLDLYVWGLDLYV 40

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CC 1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
DR EMBL: AF131057; AAF31017.1;
DR HSP; P29274; IMMH.
DR InterPro: IPR000276; GPCR_Phosph.
DR Pfam: PF00001; 7tm 1; 1
DR PRINTS: PS00237; GPCRPHOSPN.
DR PRINTS: PR01565; NEUROMEDINUR.
DR PRINTS: PR01570; NPPRRECEPT.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 411 AA; 47090 MW; 4584862A44150 CPO64.

Query Match
Best Local Similarity 24.1%; Pred No 2 10;
Matches 90; Conservative 50; Mismatches 142; Indels 57; Gaps 12.

CY 22 WPTIIFALLVA-VLVGFVSNVWVIGIILHNAMKFSFMSHLSLNLADLSLLFSAP 80
DB 116 VNFVALGESEVFTARTTFEINFEETAVTAGVYNTAAATPMAATPDKRATAT 176
CY 140 TMSVVAIVAVASLLPELPEFESTIPHHGVMTLVAVAHKMS MPRLY 104
DB 136 FIVISINWLAFAAFVLYFPPMPFSTTLYNTFGLTGTGTTGTTGTTGTTGTT 176
CY 134 PLLAPFLPLFPAPVPRAY GQPFKIPYKLEKELKELKELKELKELKELKELK 140
DB 134 PLLMATTIVVJHNSSEH RQTF VLFAPAPAPAPAPAPAPAPAPAPAPAPAP 140
CY 250 WLEPWV... - - - - - AAWTWHLFAAATATPTPTPTPTPTPTPTPTPTPTPT 150
DB 247 WLEPHVETATVGLNRPVY - - - - - LQVIA - - - - - WNTVWNTVWNTV 150
CY 238 FEREGLPQYMPW 310
DB 336 KPPAPGPPAPPW 348

RESULT 7
Q9JKN0 PRELIMINARY, PRT, 443 AA.
AC Q9JKN0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Neurokinin B receptor
GN NK3.
OS Cavia porcellus (Guinea pig)
OC Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Cavia.
CC NCBI_TaxID=10041;
PN [1]
PP SEQUENCE FROM N.A.
RA Stumm R.K., Derst C., Schaefer M.K.H., Weihe E.;
RT "Cloning and sequencing of Guinea pig NK3 receptor."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF255393; AAK49193.1;
DR InterPro: IPR000276; GPCR_Phosph.
DR Pfam: PF00001; 7tm 1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 440 AA; 49516 MW; FR48B0AF505454D CPO64.

Query Match
Best Local Similarity 23.6%; Pred No 2 10;
Matches 77; Conservative 61; Mismatches 129; Indels 46; Gaps 11.

CY 22 WPTIIFALLVA-VLVGFVSNVWVIGIILHNAMKFSFMSHLSLNLADLSLLFSAP 80

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Db 196 FTTNDFLGPTTQVTFRISSYLLPLMIISGLYMPIMPLWPQGTGVPMKESQSGPKRXT 255
 QY 237 VMLLSIAISALLWLPWVAMVWHLKAAGPAPPGGIAL-----SOVLMFSISSANPL 291
 Db 256 PLVVVVVAFASLWLPVAILL-----LKSLSVETNTLTHIVQVTAQTLAYSSSCINPL 311
 QY 292 IFLVMSEEFEE 302
 Db 312 LYAFLESEFRK 322

RESULT 13
 Q8QCM3 PRELIMINARY; PPT; 377 AA.
 ID Q8QCM3
 AC Q8QCM3
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Neurotrophin Y receptor 4
 OS Gallus gallus (Chicken)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus
 CX NCBI_TaxID=9031;
 RN [1]
 RA LUNDALL I., Boswell T., Larhammar D.;
 RP "Chicken Neurotrophin Y Family Receptor Y4: a Receptor with Equal
 RT Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DP FMR.; AF410963; AAL84163.1;
 KW Receptor.
 SQ SEQUENCE 377 AA, 42302 MW, 92656.000PPTDIFDE CPC64,

Query Match 10.0%; Score 217.5; DB 13; Length 377;
 Best Local Similarity 22.8%; Pred. No. 1.9e-09;
 Matches 68; Conservative 66; Mismatches 125; Indels 39; Gaps 8;

QY 35 LVTFTVNTLGVIGLLHNAWFKFSMHSLNLSLALSLLSLPSAPIATVSKSVMLG 94
 Db 52 VLGIQVNTLGLIAVAPQ KFTNTVNTLNLISLPLMLVCLPPIVVTWQYWIQ 109
 QY 95 WPTKSSGWFIHTMAAKELTIVVAVFVEMVAFKQVSHNNTVMSLVA----- 147
 Db 110 FVWCFTSTQCTSVTVSLSLVIAL... EPHQIINPTGPPPTISQAVIGIG 169
 QY 148 IWTVASLPLFTEWFTSTPHHESVE-----MLLVDFVAVAEFMSMPKLY 193
 Db 161 VWTIATLMSLFLUTSLSLSLVLELHSHIMNFYSYKAIIDSNP--SEQHPLIYTTI 217
 QY 194 PLLAPGLPFAFSE-----YFWPAVQCFPPPTSTKTONLNFCEPQVTVMLL 240
 Db 218 LLQVCILPFIILCYLPIYLPLQPPHWFSEYENPAVCLPRINILLASWVAFAVCW 277
 QY 251 LPWVAMLVW-WHLKAAGPAPPGGIALSOVLMFSISSANPLIFLVMSEEFREGKGV 307
 Db 278 LPLHVTNTVDWNYKIISPCCHNLIFSLCHLVAMATCTVNPVIYGLNFKKVEKSL 335

RESULT 14
 Q8WPA2 PRELIMINARY; PPT; 361 AA
 ID Q8WPA2
 AC Q8WPA2
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Allatostatin receptor RAP
 OS Bombyx mori (Silk moth)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Bombycoidea; Bombycidae; Bombyx.
 CX NCBI_TaxID=7031;
 RN [1]

PP SEQUENCE FROM N.A.
 RC STRAIN=LYON 203 BA/LYON 300 AB;
 RX MEDLINE=21601656; PubMed=11590150;
 PA Secher T., Lenz G., Cazzamali G., Sorensen C., Williamson M.,
 RA Hanser G.N., Svane P., Grimelikhuitzen C.J.P.;
 RT "Molecular Cloning of a Functional Allatostatin Gut/Brain Receptor and
 KI an Allatostatin Receptor from the Silkworm Bombyx mori";
 PL J. Biol. Chem. 276:47052-47060(2001)
 DR EMBL; AF303370; AAL47056.1;
 DR EMBL; AF303368; AAL47056.1; JOINED.
 DR EMBL; AF303369; AAL47056.1; JOINED.
 DP FMR.; AP254742; AAG444631.1;
 DP InterPro: IPR002106; AA-PNA ligaseII.
 DP InterPro: IPR0000274; GPCR_Phospn.
 DP Pfam: PF00001; 7tm1.1;
 DR PRINIS; PR00237; GPCR_HODOPSIN.
 DR POSITE; PS00339; AA_PNA_LIGASE II; UNKNOW 1.
 DE POSITE; PS00337; G-PROTEIN RECF1; UNKNOW 1.
 DE POSITE; PS00342; G-PROTEIN RECF1_2; 1.
 KW Receptor.
 SQ SEQUENCE 361 AA, 40478 MW, 63028.946PC3010A CPC64;

Query Match 9.9%; Score 214.5; DB 5; Length 361;
 Best Local Similarity 24.6%; Pred. No. 2e-09;
 Matches 84; Conservative 52; Mismatches 141; Indels 65; Gaps 12;

QY 25 IIPALLVAVCLGVGVLGIGILLHNAWFKFSMHSLNLSLALSLLSLPSAPIAT 94
 Db 44 VDFPGFVIGVGLVGNALVVLVAAN FGMSTTNLLIINLAVADLLVFCVDFET 101
 QY 85 AYSFVSMGLTWPFVSSDFHTCMAAKSLTIVVAVFVEMVAFKQVSHNNTVMS 144
 Db 102 EYWPFPWFETQWYVYVQVFIIVTAHAGVILVLSLPSMAVTHIAKELF 159
 QY 145 LVA---IWTVASLPLP-----EWFSTPHHESVEMLVDFVAVAEFMSMSEKLY 193
 Db 160 LLATATVWVILTTATPVGICHGESEYSEYFNHSSCV-----FLEEG--Y 204
 QY 194 PLLAPGLPFAFSE-----YFWPAVQCFPPPTSTKTONLNFCEPQVTVMLL 240
 Db 205 SKLPQMSFLSYVPIALISVLVWCMTPVWFAFGGVAFSPSP...PVTEMV 261
 QY 241 SLALISALLGLFEWAVLWVHLFAAGAPAECEFA LSVNMFSTESANPLIFLVM 296
 Db 262 VVVVFAVWVPICLL VKALNPYHITYFTVTAQVCHVLAWMSQVNFVAVL 317
 QY 297 SEFPPELFLVWKKMTYK-----FTVSPSEIIPATNS 330
 Db 318 SENFPVAPP---FVNYCPPPYNDGFSRPPCATFTPTPTNSNS 356

RESULT 15
 Q8JF40 PRELIMINARY; PPT; 385 AA
 ID Q8JF40
 AC Q8JF40
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Somatostatin subtype 5 receptor.
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 PA O'Carroll A.-M.;
 RT "Cloning, sequence and tissue distribution of the gene encoding a
 PL mouse somatostatin subtype 5 receptor";
 PL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 CC - SURCELLULAR LOCATION INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC - SIMILARITY BELONGS TO FAMILY 1 OF 5-RELATED COUPLED RECEPTORS.
 DR EMBL; AF268067; AAF72547.1; --

```
DR HSPD; P02699; 1F88.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHH00FSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
FW Glycophorin type-1 receptor_Glycophorin, receptor; Transmembrane
SQ SEQUENCE 365 AA; 4/489 MW; 4F01140E0604F85 CRC64;

Query Match          0 0%, Query 214 5, DR 11, Length 385,
Best Local Similarity 24 0%, Pred No. 3 4e-09;
Matches 89; Conservative 67; Mismatches 164; Indels 51; Gaps 16;

QY 17 SSSQW -----ETIIPALIVAVCLVSEVENLTVGILHNAWKPSPMHSLLI 64
RB 42 SSSHEKSLVTVSEPKAPAVLVVIVLVTVSGTILVITVVLFYAFME TVTNVYI 99
QY 45 LNLSLALSLILFSAPIEATAYSEKSWLIGMEVCKSSDWFIHTMAAKSLTIIVVAVKVF 124
RB 100 LNLAVGV-LPWLGLPFLALGNVSWPESLEP-----LWTLGGINGFTSI----PCL 150
QY 125 MYADSEAKGVSH NYTWS VLVAIWTVAGLLILFEPWFFSTIRHHGVEMCL 175
RB 161 MVMGVSEYLVAVHFESEAPSPPEPPAPYASAAVWVPEGLMPTILVPAVQ-ETWNTTN 208
QY 170 VLVAVAVSEPMVEGKILHLLAFGLLFFASFPWPAVDYTKFFSTNLEFNQIPSKGV 235
RB 200 LSWPEVRLWDAFITYTETVIGFEPFLIVLCYLLIVVWVAGMPVGSRRPRSPRPV 268
QY 236 TWMLLSIALISALLMPEWVAMLVWHLYAGAPAP--GEFIALSQVLMFSTISANPLIF 293
RB 263 TMTVTVVTVVTVVGVGLPPEI VNVVLAFTEPEEFTSAGLVFEVTVLVYANSCANNLY 326
QY 294 LVMSEFPPEGLGVWWMITYFDPTVSEQFTPAKNSCLPDVWVSPSPDASIDEPFPYDS 353
RB 327 GPLSLNFPASPP---FALCIPETVAVED-----ADAIEFPPEPKSGPPQT--TLPTP---S 373
QY 354 SPSSGKGKTK 364
RB 374 CFANGLMQTSR 384
```

Search completed: January 28, 2003, 11:51:30
Job time : 38 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 11:49:21, Search time 21 Seconds
(without alignments)
1858.599 Million cell updates/sec

Title: US-09-828-432-3

Perfect score: 2167

Sequence: 1 MNVSFAHHPAGGYLPDSQ.....QNDPIPWEDHQTGEGVK 406

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 293224 seqs, 36134422 residues

Total number of hits satisfying chosen parameters. 293224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 265 | 12.2 | 397 | JC5949 | galanin receptor 2 |
| 2 | 262.5 | 12.1 | 349 | I59336 | galanin receptor 1 |
| 3 | 236.5 | 10.9 | 423 | B40470 | glucocorticoid-ind |
| 4 | 236 | 10.9 | 444 | T27866 | hypothetical prote |
| 5 | 231 | 10.7 | 407 | S23510 | neurokinin 1 recep |
| 6 | 229 | 10.6 | 419 | A46226 | somatostatin recep |
| 7 | 227 | 10.5 | 407 | A34357 | neurokinin 1 recep |
| 8 | 227 | 10.5 | 407 | S20304 | neurokinin 1 recep |
| 9 | 224.5 | 10.4 | 410 | A44081 | kappa-type opioid |
| 10 | 224 | 10.3 | 465 | JQ1517 | neurokinin 3 recep |
| 11 | 223.5 | 10.3 | 443 | D40470 | glucocorticoid-ind |
| 12 | 221 | 10.2 | 395 | S55524 | neurokinin 3 recep |
| 13 | 221 | 10.2 | 407 | JQ1274 | neurokinin 1 recep |
| 14 | 221 | 10.2 | 452 | A34916 | neurokinin 3 recep |
| 15 | 218 | 10.1 | 357 | JC7319 | probable allatosta |
| 16 | 217 | 10.0 | 363 | I48261 | angiotensin II rec |
| 17 | 216.5 | 10.0 | 390 | JH0374 | tombasin receptor, |
| 18 | 216.5 | 10.0 | 402 | I56595 | neurokinin 2 recep |
| 19 | 215.5 | 9.9 | 384 | S00516 | neurokinin 2 recep |
| 20 | 215.5 | 9.9 | 390 | A36737 | neurokinin 2 recep |
| 21 | 214 | 9.9 | 363 | JC2543 | angiotensin II rec |
| 22 | 214 | 9.9 | 384 | S20303 | neurokinin 2 recep |
| 23 | 211.5 | 9.8 | 375 | I39182 | neuropeptide Y/pep |
| 24 | 211 | 9.7 | 343 | A44922 | angiotensin II rec |
| 25 | 210.5 | 9.7 | 398 | JQ1059 | neurokinin 2 recep |
| 26 | 208.5 | 9.6 | 375 | G02300 | pancreatic polypep |
| 27 | 208.5 | 9.6 | 444 | A42685 | cholecystokinin re |
| 28 | 207 | 9.6 | 428 | S30508 | probable G protein |
| 29 | 206.5 | 9.5 | 491 | C40470 | glucocorticoid ind |

ALIGNMENTS

RESULT 1

JC5949

galanin receptor 2 - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003

C:Accession: JC5949

R:Bloomquist, B.T.; Beauchamp, M.R.; Zhelnin, L.; Brown, S.E.; Gore-Willse, A.R.; Gregor,

Biochem. Biophys. Res. Commun. 243, 474-479, 1998

A:Title: Cloning and expression of the human galanin receptor GalR2.

A:Reference number: JC5949; MUID:98153789; PMID:9480833

A:Accession: JC5949

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-387 <BL0>

A:Cross-references: GB:AF040630; NID:30321759; PIR:AC03634.1; PIR:09021760

C:Superfamily: vertebrate rhodopsin

Query Match 12.2%; Score 265; DB 2; Length 387;

Best Local Similarity 26.7%; Pred No 1 3e-13;

Matches 85; Conservative 53; Mismatches 154; Indels 26; Gaps 9;

QY 12 GYLEDSCCTFTTIPALLVAVCLVGVGHLCVIGILLHNWGFQPMVHSIINISLAD 71

DB 19 GQWHPD-----AVIVPLIFALIFVGVNTLVLAVALRGQ--QAVSTIFLNLGVAP 71

QY 72 LSLILFSAFIPATAYSKSVWELGWFCVSSFWHTTMAAFSLTIIVVAVKVFVASQPA 131

DB 72 LCFILCCVFPQNTIYLDGWVFGSLCKAVHFLFLTMHASSFTLAAYSLDRILAYPL 131

QY 132 KQVSHNNTIWSVLA---IWTVASLLPLPEWFFSTIPHHE--GVEMCI VIVPAVAFEEM 186

DB 132 HSFELP--TTHALAAIGLILWLSLLFSST YLVVYVGSJLANLYTHTANSAPFEEM 187

QY 187 S-----MFGFLIFLAFGLPLFASFYFPAVDQCFKSTCTONLPNIPSKQVWMLSS 242

DB 188 DICTVFESYLLFVLGLTYAFTIFILFAVTPV-AAGSGAPPAP- SVTRNLLIV 241

QY 243 AIIISALLWLPFWVWLWVWLHKAAGPAPQGFIALSQVLMFSSISANPLFLVMSEEFRE 302

DB 242 AALFCLCWVPHALLICVWFGQFPLTPATYALFILSHINVSANSCNFIIVAVVCTPFR 301

QY 303 GLKGVWVWMTTFPPTVS 320

DB 302 GPRTICAGILGPAPGRAS 319

RESULT 2

I59336

galanin receptor 1 - human

C:Species: Homo sapiens (man)

C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2003

C:Accession: I59336; JC5949; G01765; G02528

QY 142 MSVLVAITVALLPLPEWFSTIRHH-----EGVEMCLVDVPAVABE----- 184
Db 162 ALCFYIIIIASCIPIVG-----RMHGIYVDFIMEKRSTCAITLTATAEATPTMARTY 214
QY 185 FM--SMFGKLYPLLAFLGLFFAFYFWRAYDOCKKPGTKT---ONLRNQ-----IR--- 231
Db 215 FMTFVFGVVLPL--GISVLYGLMLPKLMDMPRPGNSQSGGRNLTRDSSGSIIRPP 271
QY 232 --SKQVTVMLLSTAILLALPEVAVLWVHLKAAGFAPDGGFI----- 275
Db 272 EATVAAVPTPLVGLVITWALCWPLNVCFP-----MSGIAYEPVLVSHGVIMVIVQ 325
QY 276 ALCOVLMFSGISANPLIFVMSSEEPREGKLVGKWKMITX 314
Db 326 IACQVLAAYTUSCLNPLILYALMSQSPEGFIPVWKMINK 364
RESULT 5
S23510
N:Altkin 1 receptor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 19-May-2000
C:Accession: S23510; S19198
R:Gorbulev, V.; Akhundova, A.; Luzius, H.; Fahrenholz, F.
Biochim. Biophys. Acta 1131, 99-102, 1992
A:Title: Molecular cloning of substance P receptor cDNA from guinea-pig uterus.
A:Reference number: S23510, MUID:92256498, PMID:1374648
A:Accession: S23510
A:Molecule type: mRNA
A:Residues: 1-407 <GPP>
A:Cross-references: EMBL:X64323; NID:g49565; PIDN:CAA45608.1; PID:g49566
C:Superfamily: G protein-coupled receptor; glycoprotein; transmembrane protein
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
F:32-55/Domain: transmembrane #status predicted <TM1>
F:69-89/Domain: transmembrane #status predicted <TM2>
F:117-128/Domain: transmembrane #status predicted <TM3>
F:149-169/Domain: transmembrane #status predicted <TM4>
F:196-217/Domain: transmembrane #status predicted <TM5>
F:250-280/Domain: transmembrane #status predicted <TM6>
F:289-308/Domain: transmembrane #status predicted <TM7>
Query Match 10.7%, Score 231, DB 2; Length 407;
Best Local Similarity 22.1%; Pred. No. 7.3e-11;
Matches 86; Conservative 80; Mismatches 159; Indels 64; Gaps 13;
QY 22 WETIIPALLVAVCIY-GEVGNLCVIGIILLHNAWKPKSMTHSLNLSLADLSLLPSAP 80
Db 30 WCIVLWAAAYTVIVVTSVGVNVMWIL--AHKRMETVTNYFLVNLAFASMAAFNTV 87
QY 81 IPATAYSKVMDLGMFVCKSSDWFIHTCMAAKSLTIIVVAVKCFMVASDPAKQVSHNYT 140
Db 88 VFTTAVIREWNYGLFYCKFNHFPPIAAVPAIYSMTAVAFDRYMAIIHPL-QPRLSATA 146
QY 141 IWSVLVAITVALLPLPEWFSTIRHHGEVEMCLVDVPAVABEPMFGKLY----- 193
Db 147 TKVVICVIVLWALLAFPGQYYSITETTPGRVWCWIEWPSHPDK---IYEKVVHICVTVL 203
QY 194 ----PLLAFLPLFASVYFAYDOCKKRGTKTCLNLRNQLRSKQVTVMLLSIAIIS-AL 248
Db 204 IYFLPLVLIGYATVVGITLWAS-----RIPGSDSDRYHEQVSAKKVVKWIVVCTFAI 259
QY 249 LWLPEVAVLWVW----HLKAAGFAPPQGFIALSOVLVMSISSANELLIFLWSEEBREG 303
Db 260 CWLPHIPELLVPINPLVLYK---KFIQCVLAIWMLAM-SSTWYNPIIYCLINDRPLFG 315
QY 304 LKGVWV-----WMLTKKPTVTSBESQTPAGNSEGLPKD 336
Db 316 FPAHFCOFPFLSAAYVEGLEMYSTYFQTGGSVYKVSLETTIS-----TVVGAHEEDPBE 371
QY 337 VPSPEPASIPKEKPSPPSGKGTAKA 365

Db 372 GPK-ATPSSLLTSGSRNSRNSKTVTESS 399
RESULT 6
A46226
N:Somatostatin receptor 3 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18 Nov 1994 #text_change 24 Nov 1999
C:Accession: A46226; S32501
P:Yanada, Y.; Reisine, T.; Law, S.F.; Ihara, Y.; Kubota, A.; Kagimoto, S.; Seino, M.; Sei
Mol. Endocrinol. 6, 2136-2142, 1992
A:Title: Somatostatin receptors, an expanding gene family: cloning and functional charact
A:Reference number: A46226, MUID:93149121, PMID:1337145
A:Accession: A46226
A:Molecule type: DNA
A:Residues: 1-418 <YAM>
A:Cross-references: GB:M96738; NID:g338438, FID:AAA62522.1, PID:g338490
A:Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIPI:213690)
R:Corneiss, J.D.; Demchishyn, L.L.; Seeman, P.; van Tol, H.H.M.; Strikant, C.F.; Kent, G.
FEBS Lett. 321, 279-284, 1993
A:Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays prefer
A:Reference number: S32501; MUID:93238970; PMID:8097479
A:Accession: S32501
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-418 <COR>
C:Genetics:
A:Gene: GDB:SSTR3
A:Cross-references: GDB:134187; OMIM:182453
A:Map position: 22q13.1-22q13.1
A:Introns: #status absent
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro
F:81-106/Domain: transmembrane #status predicted <TM1>
F:118-139/Domain: transmembrane #status predicted <TM2>
F:159-181/Domain: transmembrane #status predicted <TM3>
F:203-233/Domain: transmembrane #status predicted <TM4>
F:255-282/Domain: transmembrane #status predicted <TM5>
F:289-316/Domain: transmembrane #status predicted <TM6>
F:317-330/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:316-317/Disulfide bonds: #status predicted
F:311-351/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status
F:321/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status predict
F:256/Binding site: phosphate (Thr) (covalent) (by CAMP-dependent kinase) #status predict
F:412/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
Query Match 10.6%, Score 229, DB 2; Length 418;
Best Local Similarity 23.4%; Pred. No. 1.1e-10;
Matches 83; Conservative 63; Mismatches 160; Indels 48; Gaps 11;
QY 25 IIPALLVAVLVGEVGNLCVIGIILLHNAWKPKSMTHSLNLSLADLSLLPSAPIRAT 84
Db 46 LIPVLVAVLVVGLGNSLVIVVLRHT--ASPSVTRVILLALAD ELVMLGLPLFA 144
QY 85 AYSKSVMDLGMFVCK-----SSDWFIHTCMAAKSLTIIVVAVKCFMVASDPAKQV 134
Db 103 QNALSYPPFGLSLMCLVMAVDGINQFTSFCLIVMSVDRLVAVVHTRSAKMTAEVAF 161
QY 135 SIHNTVMSVLVAITVAVSLPLPEWFSTIRHHGEVEMCLVDVPAVABEPMFGKLY 194
Db 162 -----TVSAAVVAVASAVVLEPVVVFSGV--PRGSTCHMQWPEPAANWPAAGFIITYA 211
QY 195 LLAFGLPLFFASVYFWRAYDOCKKRGTKT---QMLFNQIPRSKQVTVMLLSIAIISALLNL 259
Db 212 ALGFFGLVAVLCVLLIVVVPVSAQFPVMAVATGVPFSEPAVAVVAVVAVLEFV 271
QY 252 PEVAVLWVWHLKAAGFAPPQ-----GFIALSOVLVMSISSANELLIFLWSEEBREG 307
Db 272 PEVVLNI---VNVVCLPFEFAFFGLYFLVAVL-PYAVSANTILYGLFYPFLVAF 325
QY 308 WKWMLTKKPTVTSBESQETPAGNSEGLDKVTSPESPASIDKEKPPSSPSCKGK 361

Db 326 ---RVLLPSPSRVPQPTVGP-----PEKTEEDE-----EEDGESPEGGKX 368

RESULT 7

A14357
neurokinin 1 receptor - rat
N:Alternate names: NK-1 receptor, substance P receptor
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 19-May-2000
A:Accession: A34692; A34357; A40089
R:Heitsch, A.D.; Dykema, P.E.; Krause, J.E.
J. Biol. Chem. 266, 4366-4374, 1991
A:Title: Organization, structure, and expression of the gene encoding the rat substance P receptor
A:Reference number: A34692, MUID:31154239, PMID:1705552
A:Accession: A34692
A:Molecule type: DNA
A:Residues: 1-407 <HEP>
A:Cross-references: GR:M34751
R:Yokota, Y.; Sasaki, Y.; Tanaka, K.; Fujiwara, T.; Tsubota, K.; Shigemoto, R.; Kakinaka, J. Biol. Chem. 264, 17640-17652, 1989
A:Title: Molecular characterization of a functional cDNA for rat substance P receptor
A:Reference number: A14357, MUID:20036923, PMID:2478537
A:Accession: A14357
A:Molecule type: mRNA
A:Residues: 1-407 <YOK>
A:Cross-references: GR:356037, NID:3207651, PID:AAA43175.1; PID:3207052
R:Heitsch, A.D.; Krause, J.P.
Science 247, 959-962, 1990
A:Title: Molecular characterization of a functional cDNA encoding the rat substance P receptor
A:Reference number: A40089, MUID:20010991, PMID:2154952
A:Accession: A40089
A:Status: preliminary
A:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 10.5%, Score 227, DB 2, Length 407,
Best Local Similarity 22.9%, Pred. No. 1.5e-10;
Matches 89; Conservative 71; Mismatches 165; Indels 64; Gaps 13;
QY 22 WPTIIPALLVAVCLV GFVGNLCVIGILLINAWKPFPSMHSILNLSLRLSLLLSPAP 80
DB 30 WQVLWAAATVIVTVSVGNVWVWILL--AHKMRITVTVNVLNLAFAACMAAFNTV 87
QY 81 IPATAYSKSVMDUGWVFVCHSSWFHTCMAYSLTIIVVAVKCFMYADPAQVSIHNYT 140
DB 88 VNFTYAVINWVYVYGFYCKPHNFPIAALFASISMTAVAFDRYMAIIHPL-QPRLSATA 146
QY 141 IWSVLVAIWTVASLLPLPEWFFSTIRHHGVEMCLVDVPAVAEERMSFGKLY----- 193
DB 147 TKVIVFVWVIALLLAFPGGYSTTETMSPVVCWIEWP---EHNRYEKAYHLCVTVL 203
QY 194 ---PLLAFLGLPLFPASFPWPAVDQCKFKFTKTLNLPQIPKQVTVWMLQALIS 248
DB 204 IYELPLLVIGYAVTVVGITLWAS---EIPGDSRVRHGVSAFPAKVMWIVVCTEAI 259
QY 249 LWLPEWVAWLWVW----HLKAAGPAPPGFIALSQVLMFSSISANPLIFVMSEEPFG 303
DB 260 CWLPHVFFLLVYHPELYL---VFICQVYLA-SWKLAWSTWYRPIYCCLDPPPLG 315
QY 304 LKGVWK-----WMTKPTFTWSKSTJA 368
DB 316 FKHAFFCCPFIAGRYEGLEMKSTPYLOTSSVYVKSPIETTIS---TVVGAHEEPDE 371
QY 337 VPSPEPASIPPEKPPSPSSSGVGFTEFA 365
DB 372 GPK-ATPSSSLDTSSGSSPNSKMTKSS 399

RESULT 8

S20304

neurokinin 1 receptor - mouse

N:Alternate names: NK-1 receptor; substance P receptor
C:Species: *Mus musculus* (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 10-May-1995 #text_change 6-Jun-1999
A:Accession: S20304, I56216; I71044
R:Sundelin, J.B.; Provvedini, D.M.; Wahlstedt, C.R.; Laurell, H.; Fahl, G.; Persson, L.
Eur. J. Biochem. 203, 625-631, 1992
A:Title: Molecular cloning of the murine substance P and substance P receptor genes
A:Reference number: S20304, MUID:20117043, PMID:1370937
A:Accession: S20304
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-407 <SUN>
A:Cross-references: GB:X62934, NID:354296, PID:CAA44703.1; PID:361407
R:Book, G.A.; Elliott, D.; Marwalli, A.; Blum, A.M.; Sanfey, M.; Tybirk, P.; Wahlstedt, C.R.
J. Immunol. 152, 1830-1835, 1994
A:Title: Molecular evidence that granuloma T lymphocytes in murine granuloma contain substance P receptors
A:Reference number: I56216, MUID:94165478, PMID:8120392
A:Accession: I56216
A:Status: preliminary; translated from GR/PMPL/DBPL
A:Molecule type: mRNA
A:Residues: 63-390 <COOL>
A:Cross-references: GB:L27826, NID:9450286, PID:AAA7041.1; PID:118127
A:Experimental source: tissue brain
A:Accession: I71044
A:Status: preliminary; translated from GR/PMPL/DBPL
A:Molecule type: mRNA
A:Residues: 63-390 <COOL>
A:Cross-references: GB:L27826, NID:9450286, PID:AAA7041.1; PID:118127
A:Experimental source: tissue granuloma
C:Superfamily: neurokinin 1 receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 10.5%, Score 227, DB 2, Length 407,
Best Local Similarity 22.6%, Pred. No. 1.5e-10;
Matches 88; Conservative 72; Mismatches 165; Indels 64; Gaps 13;

QY 22 WPTIIPALLVAVCLV GFVGNLCVIGILLINAWKPFPSMHSILNLSLRLSLLLSPAP 80
DB 30 WQVLWAAATVIVTVSVGNVWVWILL--AHKMRITVTVNVLNLAFAACMAAFNTV 87
QY 81 IPATAYSKSVMDUGWVFVCHSSWFHTCMAYSLTIIVVAVKCFMYADPAQVSIHNYT 140
DB 88 VNFTYAVINWVYVYGFYCKPHNFPIAALFASISMTAVAFDRYMAIIHPL-QPRLSATA 146
QY 141 IWSVLVAIWTVASLLPLPEWFFSTIRHHGVEMCLVDVPAVAEERMSFGKLY----- 193
DB 147 TKVIVFVWVIALLLAFPGGYSTTETMSPVVCWIEWP---EHNRYEKAYHLCVTVL 203
QY 194 ---PLLAFLGLPLFPASFPWPAVDQCKFKFTKTLNLPQIPKQVTVWMLQALIS 248
DB 204 IYELPLLVIGYAVTVVGITLWAS---EIPGDSRVRHGVSAFPAKVMWIVVCTEAI 259
QY 249 LWLPEWVAWLWVW----HLKAAGPAPPGFIALSQVLMFSSISANPLIFVMSEEPFG 303
DB 260 CWLPHVFFLLVYHPELYL---VFICQVYLA-SWKLAWSTWYRPIYCCLDPPPLG 315
QY 304 LKGVWK-----WMTKPTFTWSKSTJA 368
DB 316 FKHAFFCCPFIAGRYEGLEMKSTPYLOTSSVYVKSPIETTIS---TVVGAHEEPDE 371
QY 337 VPSPEPASIPPEKPPSPSSSGVGFTEFA 365
DB 372 GPK-ATPSSSLDTSSGSSPNSKMTKSS 399

RESULT 9

A44081

kappa type opioid receptor - human
C:Species: *Homo sapiens* (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 6-Apr-1999
C:Accession: A44081
R:Xie, G.X.; Miyajima, A.; Goldstein, A.

100

Db 348 KPFPAGEKPAFFW 360

RESULT 15

JC7319
 Probable allatostatin receptor-2 fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 08 Sep 2000 #sequence_revision 16 Sep 2002 #rev_date 02-Aug-2002
 C:Accession: JC7319
 R:Lenz, C.; Williams, M.; Grimmelikhuijzen, C.J.P.
 Biochem. Biophys. Res. Commun. 273, 571-577, 2000
 A:Title: Molecular cloning and genomic organization of a second probable allatostatin receptor
 A:Reference number: JC7319
 A:Accession: JC7319
 A:Molecule type: mRNA
 A:Residues: 1-357 <LEN>
 A:Cross-references: GB:AF25352
 C:Comment: This receptor, belonging to the insect allatostatin neuropeptide family, which is a transmembrane glycoprotein.
 C:Genetics:
 A:Gene: dar-2
 A:Map position: right arm of chromosome 3, 98D-E
 A:Introns: 180/3; 273/3; 326/3
 C:Superfamily: endothelin receptor B
 C:Keywords: extracellular protein; glycoprotein; neuropeptide; transmembrane protein

Query Match 10.18; Score 218; DB 2; Length 357;
 Best Local Similarity 25.18; Pred No. 6 Re-10;
 Matches 78; Conservative 57; Mismatches 132; Indels 44; Gaps 11;

QY 13 GYLPDSQDWRTIIFALLVAVCLVGVGNLCVIGILLHNWKGKPSMIHSLILSLADLSLLEPAP 72
 Db 35 GTLP-----W--IVSFFFGVIAITGFGHLLVILWVWF--INPSTTLMETKAAADL 85
 QY 73 SLLPSAPIRATAYSKVMDLGMFVCKSDWFIHPCMAAYSLTIWVAVVPMVADSDP- 130
 Db 86 MFVILCIPPTAIDYVWYVWPYGRFWCRSVCHLVITATASIVTLMVMSIDPLAVVHPDR 145
 QY 131 AKQVSHRYNTIKSVLVAIWTVASLLPLFENFFSTIPHHGEMCLVDVPA----- 180
 Db 146 SRMRTENITLAI-VTLMLVVLWVSPVAFTHDV---VVDYLAKEHTTYEMCT 195
 QY 181 -VAEEFMS--MFCKLYPLAFGLPLFPAGFVEMPAVDCYFFSTKTNLENCIES VAVT 236
 Db 196 FTNDFDIFGRTVYVTFISSYLLPLMLISLVWEMIMELAP-ETJVWVLPVLFEEVVT 255
 QY 237 VMLLSAIIKALKEEWVAVLWVHLKAGAPAPGPFAL--SQVLMFESISANPL 291
 Db 256 RIVVVVVIATASIMLPVQDILL--LKSLVIEINTLEKLVLTAVTADLAISSCTHRE 311
 QY 292 IFLVMSEEFRE 302
 Db 312 LYAPLSENFRE 322

Search completed: January 28, 2003, 11:51:57
 Job time : 23 secs

QY 22 WRTIIPALLVAVCLV GFVGNLCVIGILLHNWKGKPSMIHSLILSLADLSLLEPAP 80
 Db 30 WOVLVMAAAATVIVVTSVGVVWVMIIL--AHKEMRTVTVNFIPLNLAFAEASMAAFNTV 87
 QY 81 IPATAYSKSVMLGMFVCKSDWFIHPCMAAKSLTIWVAVKVCVMYASDPAKQVSIHNYT 140
 Db 86 VISTVAVRHETVYGLFYCFTHIFFPFAVAFSIYMTAVADPVMATHP-QLPLSATA 146
 QY 141 IWSVLVAIWTVASLLPLFENFFSTIRHHEGVEMCLVDVPAVAEFPMSMGKLY----- 193
 Db 147 TVVIVCVIHWIALLIAPPGQSYSTTETMPSRVVCMIEWP---EHNKTYEKVHICVTVI 203
 QY 194 -----PLLAFLGLPLFAFVFWAYDCCFPRTYQNLPNQIPSKQVTVMLLSIALIS-AL 248
 Db 204 IYFPLLVIGYATVVVGITLWAS-----EIPGSSDRYHEQVSAKRVKVMIVVVCTEAI 259
 QY 249 LMLPEWVAMLVWV-----HLKAGAPAPGPFALSQVIMFSSISNPLIFLVMSEEBREG 303
 Db 260 CWLFFHIFELLVYINPDLYLK--KFIQVYLAIMWLAM-SSTMYNPITYCCINDRFRLG 315
 QY 304 LKGVWK-----WMTTKKPTVSESQETPAGNSEGLPKD 336
 Db 316 FRIAFRCCEFISADVEGLEMKSTRVLOTQSGVYKVRLETTIS---TVVGAHEERPED 371
 QY 337 VPSPEPASIPKEKPSPPSSSGKGTKE 363
 Db 372 GPV ATPSSDILTSNACSSPSDSKTMTE 397

RESULT 14

A34916
 neurokinin 3 receptor rat
 N:Alternate names: neurotensin K receptor; NK-3 receptor
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 19-May-2000
 C:Accession: A34916
 R:Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.
 J. Biol. Chem. 265, 423-429, 1990
 A:Title: Cloning and expression of a rat neurotensin K receptor cDNA.
 A:Reference number: A34916, M312 96116113, PMID 2151106
 A:Accession: A34916
 A:Molecule type: mRNA
 A:Residues: 1-452 <SHI>
 A:Cross-references: B3 365-451, M10-5205-70, F10N-AAA41688 1; PID:3205671
 C:Superfamily: neurokinin 1 receptor
 C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 10.18; Score 201; DB 2; Length 452;
 Best Local Similarity 24.94; Pred No. 5.3e-10;
 Matches 78; Conservative 57; Mismatches 132; Indels 46; Gaps 11;

QY 22 WRTIIPALLVAVCLVGFVGNLCVIGILLHNWKGKPSMIHSLILSLADLSLLEPAP 80
 Db 70 WRIALWSLAYGLVAVAVGGLIIVMIIL--AHKEMRTVTVNFIPLNLAFAEASMAAFNTL 127
 QY 81 IPATAYSKSVMLGMFVCKSDWFIHPCMAAKSLTIWVAVKVCVMYASDPAK-QVSIHNY 139
 Db 128 INFIVGLHSEWYFGANYCRFQNFPLTAVPASIVSMTAIAVDRYMAIIDPLKPLSATAT 187
 QY 140 TWSVLVAIWTVASLLPLFENFFSTIRHHEGVEMCLVDVPAVAEFPMS--MGKLY 193
 Db 188 KIF-VIGSIWILAFLLAFPOCLYKIRKVMPTLCYVQWPEGKQHTYTHIIVILVYCF 245
 QY 194 PLLAFLGLPLFAFVFWAYDCCFPRTYQNLNQPISKQVTVMLLSIALIS-ALL 249
 Db 246 PLLIMGVTVTVIGITLWGEIPGDTCDK-----YHEQLKAKRKKVVMIVVVTFAIC 298
 QY 250 WLPSEWV-----AWLWVHLKAGAPPGPFALSQVIMFSSISNPLIFLVMSE 297
 Db 299 WLPYHVVYFILTAYQQLNFWKYI-----QQVYLA-SFWLAMSSTMYNPITYCCLN 347
 QY 298 EPEFPELKGWVW 310



Db 155 VGFWALSIAMASPVAYQRLFHDSNQTCWEHWP-----NQLHKKYAVVCTPVEGYL 208
 QY 200 LPLFASVYFVFAVDCQYPCCTKQNLNPNQIPSPQVTVMLISIAISALWLPWVAWLW 259
 Db 203 LPLILLICFYAKVLLHLHK-LKMSKSEASKYTKTQTVLVVVVVGISKLPHHVLHLW 267
 QY 260 VMLKKAAGFAFPQGP-ALSQVLMFSISSANPLIFLVMSEEPFGKLGKVMWMTTKYPP 317
 Db 268 AEF--GAPFLTPASFFFRITAHCLAYSNSVNPFIYAPLSNFRKAYKQVFKCRV----- 320
 QY 318 TVCSQETIAGNSEGLPKVPSSES 342
 Db 321 ----CNESPHGDAKE-KNRIDTPES 340

RESULT 3
 GALR_MOUSE
 ID GALR_MOUSE STANDARD, PRT, 348 AA.
 AC P56479;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Galanin receptor type 1 (GALR1-R) (GALR1).
 GN GALP1 OP GALNP1 OP GALNP
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97413411; PubMed=9271210;
 RA Wang S., He C., Maguire M.T., Clemmons A.L., Purrier P.E., Guzzi M.F.,
 PA Strader C.D., Parker E.M., Rayne M.L.;
 RT "Genomic organization and functional characterization of the mouse
 Galr1 galanin receptor";
 RL PNAS Lett. 411:225-230(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=98035873; PubMed=9367674;
 PA Jacoby A.S., Webb G.C., Liu M.L., Kofler E., Hort V.J., Fathi Z.,
 RA Bortema C.D.K., Shine J., Iismaa T.P.;
 RT "Structural organization of the mouse and human GALR1 galanin
 RT receptor genes (Galnr and Galnr) and chromosomal localization of the
 RT mouse gene";
 FL Genomics 45:430-438(1997).
 CC -!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- PTM: THREE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST
 CC ONE OF WHICH MAY BE PALMITOYLATED (BY SIMILARITY)
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL; Y15004; CA475237.1;
 CC EMBL; J10657; A4887748.1;
 CC EMBL; U90655; A4887748.1; JOINED.
 CC EMBL; U90656; A4887748.1; JOINED.
 CC MGI; MGI:1096364; Galr1
 CC InterPro; IPR000276; GPCR_Rhodpsn
 CC Pfam; PF00001; 7tm_1, 1.
 CC PRINTS; PP0037; GP3PPHCQPSN.
 CC PROSITE; PS00317; G_PROTEIN_RECEP_F1_1; 1

DP POSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 FT DOMAIN 1 34
 FT EXTRACELLULAR (POTENTIAL)
 FT TRANSMEM 35 55
 FT CYTOPLASMIC (POTENTIAL)
 FT TRANSMEM 56 70
 FT TRANSMEM 71 91
 FT TRANSMEM 92 109
 FT TRANSMEM 110 131
 FT TRANSMEM 132 151
 FT TRANSMEM 152 172
 FT TRANSMEM 173 197
 FT TRANSMEM 198 218
 FT TRANSMEM 219 247
 FT TRANSMEM 248 268
 FT TRANSMEM 269 270
 FT TRANSMEM 271 291
 FT TRANSMEM 292 348
 FT CARBOHYD 7 7
 FT CARBOHYD 12 12
 FT CARBOHYD 182 182
 FT DISULFID 108 186
 FT LIPID 319 319
 SQ SEQUENCE 348 AA, 39114 MW, 6525252BAAI9F9A CRC64;
 Query Match 12.4%, Score 269; DB 1; Length 348;
 Best Local Similarity 28.3%; Pred. No. 6.8e-11;
 Matches 87, Conservative 54, Mismatches 178, Indels 39, Gaps 14;
 QY 36 VGFGVNLGVIGILLHNAWKGP-SMHSILNLSLADLSLLFSAPFAPAYSKSVWDLS 94
 Db 46 MGVLGNSLVITVLARSK-PGKRSTINLFIILSLADIAYLLFCIFFCATVVALPTWVG 104
 QY 95 WFWCKSSDFHFTCAAKSLTIVVAKVCFMYASPAKQVSI-HNYTTASVLA----- 147
 Db 105 AFICK-----FIH-----YFTVSMVSIPTLAAMSVDYVAIVHSPSSSIPVSRNALLS 165
 QY 148 ---IWTVAS-LPLPEWFPSTIRHGEVE-MCLVDVPAVAEEFMSFGKLYPL--LAFG-- 199
 Db 156 VGFWALSIAMASPVAYQRLFHDSNQTCWEHWP-----NQLHKKYAVVCTPVEGYL 208
 QY 200 LPLFASVYFVFAVDCQYPCCTKQNLNPNQIPSPQVTVMLISIAISALWLPWVAWLW 259
 Db 210 LPLILLICFYAKVLLHLHK-LKMSKSEASKYTKTQTVLVVVVVGISKLPHHVLHLW 268
 QY 260 VMLKKAAGFAFPQGP-ALSQVLMFSISSANPLIFLVMSEEPFGKLGKVMWMTTKYPP 317
 Db 268 AEF--GAPFLTPASFFFRITAHCLAYSNSVNPFIYAPLSNFRKAYKQVFKCRV----- 320
 QY 318 TVCSQETIAGNSEGLPKVPSSES 342
 Db 321 ----CNESPHGDAKE-KNRIDTPES 340

RESULT 4
 GALR_MOUSE
 ID GALR_MOUSE STANDARD, PRT, 372 AA.
 AC O08726;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Galanin receptor type 2 (GALR2-R) (GALR2).
 GN GALR2 OR GALNR2.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 EX MEDLINE=97261892; PubMed=9108306;
 PA Howard A.D., Tan C., Shiao L.L., Ralyha C.C., McKee K.V.,
 PA Weinberg D.H., Feighner S.D., Cascieri M.A., Smith F.G.,

RA McGovern P., Mahle C.D., Sutherland G.P., Iismaa T.P.,
 RA Dickinson P.E., Zimanyi I.A.,
 RT "Molecular characterization, pharmacological properties and
 RT chromosomal localization of the human GALF2 galanin receptor".
 RL Brain Res. Mol. Brain Res. 58:156-169 (1998).
 RN [4]
 PP SEQUENCE FROM N.A.
 RX MEDLINE=9004861; PubMed=9930101;
 RA Kolakowski L.F. Jr., O'Neill G.P., Howard A.D., Rousard S.P.,
 RA Sullivan K.A., Feighner S.D., Sawdzargo M., Nguyen T., Kargman S.,
 RA Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
 RA Chahrouh A., Griebner R., Ng G., Jostes M.P., Chathan A.,
 RA Khoshdel H., George S.P., Smith P.G., Cowdell R.F.;
 RT "Molecular characterization and expression of cloned human galanin
 RT receptors GALR2 and GALR3".
 R: J. Neurochem. 71:2239-2251 (1998)
 CC -1- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN AND FOR GALP. THE
 CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT ACTIVATE
 CC THE PHOSPHOLIPASE C/PROTEIN KINASE C PATHWAY (VIA GQ) AND THAT
 CC INHIBIT ADENYLATE CYCLASE (VIA Gi)
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY WITHIN THE CENTRAL
 CC NERVOUS SYSTEM IN BOTH HYPOTHALAMUS AND HIPPOCAMPUS. IN PERIPHERAL
 CC TISSUES, THE STRONGEST EXPRESSION WAS OBSERVED IN HEART, KIDNEY,
 CC LIVER, AND SMALL INTESTINE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 DP EMBL: AF040610; AAC39634 1;
 DR EMBL: AF080586; AAC08671.1 1;
 DR EMBL: AF058762; AAC18118.1 1;
 DR EMBL: AF042782; AAC36587.1 1;
 DR Genbank: H0004133; GALR2.
 DR MIM: 601691;
 DR InterPro: IPR000226; GPCR_Phodpsn
 DR Pfam: PF00001; 7tm_1.1;
 DE PRINTS: P80037; GPPPHICORP0N
 DR PROSITE: PS00237; G-PROTEIN RECP FL 1; 1
 DR PROSITE: PS00262; G-PROTEIN RECP FL 2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 28
 FT TRANSMEM 29 43
 FT DOMAIN 50 60
 FT TRANSMEM 61 81
 FT DOMAIN 82 99
 FT TRANSMEM 100 121
 FT DOMAIN 122 141
 FT TRANSMEM 142 162
 FT DOMAIN 163 187
 FT TRANSMEM 188 208
 FT DOMAIN 209 237
 FT TRANSMEM 238 258
 FT DOMAIN 259 260
 FT TRANSMEM 261 281
 FT DOMAIN 282 347
 FT CARBOHYD 2 2
 FT CARBOHYD 11 11
 FT DISULFID 98 175
 SQ SEQUENCE 247 AA; 4100 MW; C52CFB93E53C47E CPO64;
 Query Match 10.2%; Score 265; DB 1; Length 387;
 Best Local Similarity 26.7%; Pred. No. 1.4e-10;
 Matches 95; Conservative 53; Mismatches 154; Indels 26; Gaps 9;
 QY 12 GGYLPSDSQDPTIIPALLVAVTGVFVNIQVIGIILHNWAKGQFDSHGIHINLSIAD 71

DB 19 GGMHPR - AVTVLLPALLFLVTVSTVLAFLPQS - CAUSTENPFLINQVAD 13
 QY 72 LSLLLSALIPATATKSKVWDLGNFKVCKSDWFIHTMAKSLTINNVVFNINSDIA 131
 DB 72 LCPILQCVPPQATVTLDGWVFGSLCKAVHFLPLTHASSFTLAAVSLRPLATRYEL 131
 QY 132 KQVSIHRYITWGVIVA...IWTVASLLFLPEWFFSTIRHIE - GVMCLVTVFAVAEEM 136
 DB 132 HSPFLP - TFRNLAIAIGLWGLSLFSGP - VSYVPSLANTVTHASAPESAM 140
 QY 187 S...MFGKYLALAPGLPLFASTFWAYVSCHECTFTNHNKSTPEFTYTWMAEL 141
 DB 188 DITTFVESVILPVNLGLTVAPTLPIVLPVAVDPAV - AAGSGASPPAF...EAVTWVWIL 141
 QY 243 ALLSALLMFLFEWAVAKVWMLFAGGAPAI - GFALSLVLMFLSSANLILILIN-EEEEE 142
 DB 242 ALVFLQWVHALLICVWFSGQFFLTPTATVALNLSHNVYANGSCVFTTVALVSHFER 142
 QY 303 GLGVWVFWMITTPPTVS 320
 DB 302 GPFTICAGLLGPAPGRAS 319
 RESULT 6
 GALR HUMAN STANDARD, PFT, 349 AA.
 ID P47231.
 AC 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 14-OCT-2001 (Rel. 40, Last annotation update)
 DE Galanin receptor type 1 (GALR1-P) (GALP1).
 GN GALP1-P (GALR1-P) (GALP1).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 PP [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE 95024044; PubMed:7524088;
 RA Habert-Ortoli E., Amiranoff B., Loquet I., Laburthe M.,
 RA Mayaux J.-F.;
 FT "Molecular cloning of a functional human galanin receptor".
 PL Proc. Natl. Acad. Sci. U.S.A. 91:9780-9783 (1994).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Ross P.C.;
 RC Submitted (MAR 1995) to the EMBL/GenBank/CCDS databases.
 RN [3]
 PP SEQUENCE FROM N.A.
 RC TISSUE=Small intestine;
 RX MEDLINE-98086300; PubMed 9425310;
 RA Lorimer D.D., Markowski K., Benya P.V.;
 FT "Cloning, chromosomal location, and transcriptional regulation of the
 FT human galanin 1 receptor gene (GALR1R)".
 PL Biochem Biophys Res. Commun. 241:558-564 (1997).
 RN [4]
 PP SEQUENCE FROM N.A.
 RX MEDLINE-99035873; PubMed-9367674;
 RA Jacoby A.S., Webb G.C., Liu M.L., Kofler R., Hart V.J., Fathi Z.,
 RA Berman C.P., Shino T., Iismaa T.P.,
 FT "Structural organization of the mouse and human GALF1 galanin
 FT receptor genes (Galnt and GALNP) and chromosomal localization of the
 FT mouse gene".
 RT Genomics 45:442-458 (1997).
 CC -1- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- PTM: THREE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST
 CC ONE OF WHICH MAY BE PALMITOYLATED.

FT DOMAIN 258 259 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 260 280 7 (POTENTIAL).
 FT DOMAIN 281 370 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 6 6 N-LINKED (GLCNAC...) (POTENTIAL).
 FT DISULFID 95 172 BY SIMILARITY.
 FT LIPID 308 308 PALMITATE (BY SIMILARITY).
 FT DOMAIN 218 225 POLY-ALA.
 FT CONFLICT 54 54 R -> S (IN REF. 3).
 FT CONFLICT 127 127 R -> Q (IN REF. 2).
 FT CONFLICT 183 183 A -> P (IN REF. 2).
 FT CONFLICT 311 311 R -> C (IN REF. 2).
 SQ SEQUENCE 370 AA; 40410 MW; CESB3956147AFAD4 CRC64;

 Query Match: 12.0%; Score 261; DB 1; Length 370;
 Best Local Similarity 24.4%; Pred. No. 2.4e10;
 Matches 87; Conservative 53; Mismatches 155; Indels 60; Gaps 12;

 QY 26 IFALLVAVCVGVGNLCV-GILLH--NAWKCKFSMIHSLIINLSLADLSLLPSAPIR 92
 DB 20 VFVIFALIFLGMVGNGLVAVLLOQFSAMQEFRTTDLFILNLAVADLCFLCCVPFQ 79
 QY 83 ATAYSKSVWELGMPVCKSSDWFIHTCNAAKSLTIIVVAKVCFMYASDDPAKQVSIHN-VYI 141
 DB 80 AAVITLDAMLFGAFVCKTVHLLIYLTMYASSFTLAASVLDRLVAVBHPPLRSALFTPRNA 139
 QY 142 WSVLVAIVTWNASLLPPEW FFSTIRHHEGVEMCL-----VDVPAVAEEFNSMEFG 190
 DB 140 RAAVGLVWLLAALFSAFYLSTYGTVR-YGALELCVPWEDARRALDVATFAA-----G 192
 QY 191 KLYPL-----LAFGLPLFFASFYFWPAVDQCKKGTGTQNLQNLQIRSKQVTVMILSTATIS 246
 DB 193 YLLPVAVUSLAYGPTLCF-----LMAAVGPA--GAAAGAAPPPATGPAGRAM-LAVAALY 244
 QY 247 ALLMLPWWVWLVWHLKAAGPAPPGQFIALSOVLMSISSANPLIFLWMSFEFREGKLG 306
 DB 245 ALCWGPHHALILCWYGEFAFATYACRLASHCLAYANSCNPLVYSLASHPFRARPER 304
 QY 307 VWKMWITKKPTVSESQETTAGN-----SEGLPKVPSPESPASIPKEKP 352
 DB 305 LW-----PCGPPPHHHHPALPFPVCPASSGAGYGGAPP 342

 RESULT 8
 GALT MOUSE
 ID GALT MOUSE STANDARD; PRT; 370 AA.
 AC O88853;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Galanin receptor type 3 (GAL3-R) (GALR3).
 GN GAL3 OR GALNR3.
 OS Mus musculus (Mouse).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 CC Mammalia, Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 PP SEQUENCE FROM N A
 RC STRAIN=129/SV;
 RA Kolakowski L.F., Jr., O'Neill G.P., Howard A.D., Broussard S.R.,
 RA Sullivan P.A., Feigenbaum S.D., Sawdzargo M., Nguyen T., Yargman S.,
 RA Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
 RA Chateaufort A., Coulombe N., Ng G., Johnson M.P., Tharian A.,
 RA Khoshbouei H., George S.F., Smith P.G., O'Dowd B.F.,
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF042783; AAC36588.1; -;
 CC MGD; MGI:1329003; Galr3.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm1; 1.
 DE PRINTS; PR00237; GPCRPHOTOPSN.
 DE PROSITE; PS00337; G-PROTEIN RECF F1_1; 1.
 DE PROSITE; PS00342; G-PROTEIN RECF F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Lipoprotein; Palmitate.
 KW EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1 20
 FT TRANSMEM 21 41 1 (POTENTIAL)
 FT DOMAIN 42 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL)
 FT DOMAIN 79 96 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 97 118 3 (POTENTIAL)
 FT DOMAIN 119 138 4 (POTENTIAL)
 FT TRANSMEM 139 159 4 (POTENTIAL)
 FT DOMAIN 160 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 5 (POTENTIAL).
 FT DOMAIN 206 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 257 6 (POTENTIAL).
 FT DOMAIN 258 259 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 260 280 7 (POTENTIAL).
 FT DOMAIN 281 370
 FT CARBOHYD 6 6
 FT DISULFID 95 172
 FT LIPID 308 308 PALMITATE (BY SIMILARITY).
 FT DOMAIN 313 318 POLY-HIS.
 SQ SEQUENCE 370 AA; 40390 MW; D387A2FCB6D28E18 CRC64;

 Query Match: 12.0%; Score 260.5; DB 1; Length 370;
 Best Local Similarity 24.4%; Pred. No. 2.6e-10;
 Matches 87; Conservative 54; Mismatches 154; Indels 61; Gaps 12;

 QY 26 IFALLVAVCVGVGNLCV-GILLH--NAWKCKFSMIHSLIINLSLADLSLLPSAPIR 92
 DB 20 VFVIFALIFLGMVGNGLVAVLLOQFSAMQEPSTTDLFILNLAVADLCFLCCVPFQ 79
 QY 83 ATAYSKSVWELGMPVCKSSDWFIHTCNAAKSLTIIVVAKVCFMYASDDPAKQVSIHN-VYI 141
 DB 80 AAVITLDAMLFGAFVCKTVHLLIYLTMYASSFTLAASVLDRLVAVBHPPLRSALFTPRNA 139
 QY 142 WSVLVAIVTWNASLLPPEW FFSTIRHHEGVEMCL-----VDVPAVAEEFNSMEFG 190
 DB 140 RAAVGLVWLLAALFSAFYLSTYGTVR-YGALELCVPWEDARRALDVATFAA-----G 192
 QY 191 KLYPL-----LAFGLPLFFASFYFWPAVDQCKKGTGTQNLQNLQIRSKQVTVMILSTATIS 246
 DB 193 YLLPVAVUSLAYGPTLCF-----LMAAVGPA--GAAAGAAPPPATGPAGRAM-LAVAALY 244
 QY 247 ALLMLPWWVWLVWHLKAAGPAPPGQFIALSOVLMSISSANPLIFLWMSFEFREGKLG 306
 DB 245 ALCWGPHHALILCWYGEFAFATYACRLASHCLAYANSCNPLVYSLASHPFRARPER 304
 QY 307 VWKMWITKKPTVSESQETTAGN-----SEGLPKVPSPESPASIPKEKP 352
 DB 305 LW-----PCGPPPHHHHPALPFPVCPASSGAGYGGAPP 342

 RESULT 9
 GALT HUMAN
 ID GALT HUMAN STANDARD; PRT; 368 AA.
 AC O60755;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Galanin receptor type 3 (GAL3-R) (GALR3)
 GN GALR3 OR GALNP3
 OS Homo sapiens (Human)

CC Eukaryota; Mollusca; Cladocera; Stomatoda; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Hominiidae; Homo.
 CC NCBI TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9436766; PubMed=9727565;
 RA Smith K.E., Walker M.W., Actymysyn P., Bard J., Rotowsky B.,
 RA Tamm J.A., Yue W.C., Kaye P.S., Brimble T.A., Gerald C.,
 RA Jones K.A.;
 RA "Cloned human and rat galanin GALR3 receptors: pharmacology and
 RA activation of G-protein inwardly rectifying K⁺ channels.";
 RT J. Biol. Chem. 273:23521-23526(1998).
 RL [2]
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97048961; PubMed=9892121;
 RA Kakowski L.F., O'Neill G.F., Howard A.D., Proulx S.P.,
 RA Sullivan E.A., Folopet C., Sawtary M., Nguyen T., Vargan S.,
 RA Shiao L.L., Hreniak B.L., Tan C.P., Evans J., Abramowitz M.,
 RA Chateaufort A., Coulombe N., Ng G., Johnson M.P., Tharian A.,
 RA Roshchekov H., George S.F., Smith P.G., O'Leary D.F.,
 RA "Molecular characterization and expression of cloned human galanin
 RA receptors GALR2 and GALR3.";
 RT J. Neurochem. 71:2237-2251(1998).
 RL [4]
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9474120; PubMed=9428150;
 RA Iismaa T.P., Fathi Z., Hort Y.J., Iben L.G., Dutton J.L., Baker E.,
 RA Sutherland G.S., Shine J.,
 RA "Structural organization and chromosomal localization of three human
 RA galanin receptor genes.";
 RT Ann. N.Y. Acad. Sci. 863:56-63(1998).
 RL [6]
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.P.,
 RA Raquley C., Bailey J., Barlow K.F., Bates K.N., Beasley G.P.,
 RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
 RA Butler M.D., Bultun J., Carter C., Carter N.R., Chen Y., Clark G.,
 RA Clea S.M., Cobley V.E., Cole C.G., Collins P.F., Conon P.,
 RA Courtney D., Dalby M.F., Davila J.D., De A.V., Davis J., Dawson E.,
 RA Dhali P.B., Dickson C., Edwards S.G., Eickholt W.D., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gillet J.C.F., Gward M.F., Griffiths D.V., Griffiths M.D., Hall C.,
 RA Hall P.E., Hall-Tamlyn G., Heathcote P.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Karsch J., Kimberley A.M., King A.,
 RA Laird G.E., Langford C.F., Lewis M.A., Li J.C., Lloyd D.M.,
 RA Martin J.C., Mashrooqi-Mohammadi M., Matthews I.H., McCann O.T.,
 RA McLaren C., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt P., Pearce A.V., Pearson D., Phillimore P.J.C.T.,
 RA Phillips S.H., Plumb P.W., Ramsay H., Ransley V., Rogers L., Ross M.T.,
 RA Scott C.E., Shira H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Sutherland C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
 RA Vaulin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki Y., Sasaki T., Asakawa S., Fujishiro Y.,
 RA Shirani A., Shikuya K., Yoshitake Y., Aoki N., Miyayama S.,
 RA Rao P.A., Shih P., Shih C., Shih C., Shih C., Shih C., Shih C.,
 RA Norman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Pen Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Williamson P., Wu H., Yan S.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Boutin S.,
 RA Cordes M., Du Z., Fulton L., Goele D., Graves T., Hawkins J.,

PA Hinde K., Kemp K., Fariello P., Layman D., Gotsky J., Bellotti L.,
 RA Scheet P., Walker C., Wersley A., Wohldmann P., Wilson P., Wilson P.,
 RA Korf I., Bedell J.A., Hillier L., Marfat H., Wersley A., Wilson P.,
 RA Emanuel B.S., Shaikh I., Kurahashi H., Saito T., Saito T., Saito T.,
 RA McPherson H.E., Johnson A., Wong A.C., Morrow K.P., Morrow K.P.,
 RA Kim H.J., Shizuya H., Simon M.I., Dumanski J.P., Dumanski J.P.,
 RA Seroussi E., Fransson I., Tapia J., Huber C.E., Huber C.E.,
 RA Wilkerson F., Rederich A., Hartman K., Hartman K., Hartman K.,
 RA Tilahun Y., Wright H.,
 RA "The DNA sequence of human chromosome 22.";
 RT Nature 402:489-495(1999).
 RL [1]
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97048961; PubMed=9892121;
 RA Kakowski L.F., O'Neill G.F., Howard A.D., Proulx S.P.,
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 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.P.,
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 RA Butler M.D., Bultun J., Carter C., Carter N.R., Chen Y., Clark G.,
 RA Clea S.M., Cobley V.E., Cole C.G., Collins P.F., Conon P.,
 RA Courtney D., Dalby M.F., Davila J.D., De A.V., Davis J., Dawson E.,
 RA Dhali P.B., Dickson C., Edwards S.G., Eickholt W.D., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gillet J.C.F., Gward M.F., Griffiths D.V., Griffiths M.D., Hall C.,
 RA Hall P.E., Hall-Tamlyn G., Heathcote P.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Karsch J., Kimberley A.M., King A.,
 RA Laird G.E., Langford C.F., Lewis M.A., Li J.C., Lloyd D.M.,
 RA Martin J.C., Mashrooqi-Mohammadi M., Matthews I.H., McCann O.T.,
 RA McLaren C., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt P., Pearce A.V., Pearson D., Phillimore P.J.C.T.,
 RA Phillips S.H., Plumb P.W., Ramsay H., Ransley V., Rogers L., Ross M.T.,
 RA Scott C.E., Shira H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Sutherland C., Spragon L., Stewart C.A., Sulston J.E., Swann R.M.,
 RA Vaulin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki Y., Sasaki T., Asakawa S., Fujishiro Y.,
 RA Shirani A., Shikuya K., Yoshitake Y., Aoki N., Miyayama S.,
 RA Rao P.A., Shih P., Shih C., Shih C., Shih C., Shih C., Shih C.,
 RA Norman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Pen Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Williamson P., Wu H., Yan S.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Boutin S.,
 RA Cordes M., Du Z., Fulton L., Goele D., Graves T., Hawkins J.,

DB 241 VALLIWESEIPNUPK - VLLLPAPFPUPFWVLTUTTPAIONLFYHYPIIT 297
QY 256 AWLWVWHLKAGAPAPFPQFIALSQVLMFESISANPLIFLVMSEEPREGLKGVW 308
PD 258 AAUJLJNEWFI - - - - - 310
QY 309 KW 310
DB 347 RW 348

Search completed: January 28, 2003, 11:50:47
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 11:49:51 / search time 17 seconds
(without alignments)
702.689 Million cell updates/sec

Title: US-09-828-432-3

Perfect score: 2.67

Sequence: 1 MWSFAHLRFGAGYLFSEQ . . . QNDPIWEHFGQETREGVK 496

Scoring table: BLOSUM62

Gapop 10 0 , Gapext 0 5

Searched: 252574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 302574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Parents AA+
1: /cgn2_6/prodata/1/1aa/5A_OMB rep.*
2: /cgn2_6/prodata/1/1aa/5B_OMB rep.*
3: /cgn2_6/prodata/1/1aa/5A_OMB rep.*
4: /cgn2_6/prodata/1/1aa/5B_OMB rep.*
5: /cgn2_6/prodata/1/1aa/PCJUS_OMB rep.*
6: /cgn2_6/prodata/1/1aa/5A_OMB rep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

| Result No | Score | Query Match | Length | DB ID | Description |
|-----------|-------|-------------|--------|-------|--------------------|
| 1 | 270.5 | 12.5 | 371 | 4 | US-08-993-088A-9 |
| 2 | 270.5 | 12.5 | 371 | 4 | US-08-993-424B-9 |
| 3 | 269.5 | 12.4 | 346 | 4 | US-09-199-737-5 |
| 4 | 269.5 | 12.4 | 346 | 4 | US-08-993-088A-3 |
| 5 | 269.5 | 12.4 | 346 | 4 | US-08-993-424B-3 |
| 6 | 269.5 | 12.4 | 346 | 4 | US-09-058-333A-5 |
| 7 | 269 | 12.4 | 348 | 3 | US-09-513-974R-46 |
| 8 | 269 | 12.4 | 348 | 4 | US-08-993-088A-10 |
| 9 | 269 | 12.4 | 348 | 4 | US-08-993-424B-10 |
| 10 | 269 | 12.4 | 348 | 4 | US-08-540-650B-2 |
| 11 | 269 | 12.4 | 349 | 3 | US-08-513-974R-143 |
| 12 | 269 | 12.4 | 372 | 4 | US-08-665-034A-2 |
| 13 | 267 | 12.3 | 372 | 2 | US-08-606-685A-8 |
| 14 | 267 | 12.3 | 372 | 4 | US-08-993-088A-2 |
| 15 | 267 | 12.3 | 372 | 4 | US-09-993-474P-2 |
| 16 | 267 | 12.3 | 372 | 4 | US-08-665-034A-4 |
| 17 | 265 | 12.2 | 387 | 4 | US-08-993-088A-7 |
| 18 | 265 | 12.2 | 387 | 4 | US-08-993-424B-7 |
| 19 | 264 | 12.2 | 348 | 3 | US-08-513-974B-342 |
| 20 | 263 | 12.1 | 370 | 4 | US-09-199-737-2 |
| 21 | 263 | 12.1 | 372 | 4 | US-08-993-088A-20 |
| 22 | 263 | 12.1 | 395 | 4 | US-08-900-230-5 |
| 23 | 262.5 | 12.1 | 349 | 4 | US-08-993-088A-11 |
| 24 | 262.5 | 12.1 | 340 | 4 | US-08-993-424B-11 |
| 25 | 262.5 | 12.1 | 349 | 4 | US-09-540-650P-6 |
| 26 | 262.5 | 12.1 | 349 | 4 | US-08-693-308-2 |
| 27 | 262.5 | 12.1 | 351 | 3 | US-09-513-974B-344 |

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|----|-------|------|-----|---|-------------------|
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| 29 | 262 | 12.1 | 370 | 4 | US-09-058-333A-2 |
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| 34 | 229 | 10.6 | 418 | 1 | US-08-417-103-10 |
| 35 | 227 | 10.5 | 407 | 5 | FCT US92-06632-7 |
| 36 | 224.5 | 10.4 | 440 | 4 | US-08-430-286A-9 |
| 37 | 224.5 | 10.4 | 451 | 4 | US-09-430-286A-10 |
| 38 | 224 | 10.3 | 465 | 4 | US-08-090-369-1 |
| 39 | 224 | 10.3 | 465 | 4 | US-09-482-971-1 |
| 40 | 222 | 10.2 | 407 | 2 | US-09-290-000A-6 |
| 41 | 221 | 10.2 | 407 | 1 | US-08-117-965-26 |
| 42 | 221 | 10.2 | 407 | 5 | FCT US92-06632-3 |
| 43 | 221 | 10.2 | 411 | 1 | US-07-937-609-21 |
| 44 | 221 | 10.2 | 411 | 4 | US-08-029-170-21 |
| 45 | 217 | 10.1 | 353 | 1 | US-09-144-200A-2 |

ALIGNMENTS

RESULT 1

US-08-993-088A-9

Sequence 9, Application US/08993088A

Patent No. 6297855

GENERAL INFORMATION:

APPLICANT: Tan, Carina

APPLICANT: Sullivan, Kathleen

TITLE OF INVENTION: SALAMIN PEPTIDE DACT AND

TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merck & Co., Inc.

STREET: P.O. Box 2000, 125 E. Lincoln Ave.

CITY: Rahway

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/04/993,088A

FILING DATE: 18-DEC-1997

CLASSIFICATION: 530

PIPROP APPLICATION DATA:

APPLICATION NUMBER: 60/033,851

FILING DATE: 27-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Heber, Sheldon O.

REGISTRATION NUMBER: 38,179

REFERENCE/DOCKET NUMBER: 19446

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-1958

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 371 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-993-088A-9

Query Match: 12.5%, Score 270.5, 22.4, Length 371

Post Local Similarity: 24.7%, Pval. No. 1.3e-147

Matches: 92, Conservative: 61, Mismatches: 178, Indels: 4, Gaps: 11

QY 12 GGYLPSSQWPTIFALLVAVCLVGFVGM/VIGIILLHNAWKGKPMIHSLLIISLAD 71
 Db 18 GSWPE-----AVLVPEFFALIFLVGAAGNAVLAVLEFG3---QAVSTTNLFIHLGVAD 70
 QY 72 LSLLESAPATAYSGVWGLWMPVYKSDWPIHTCMAAYSLTIIVVAVFVPMVSDPA 131
 Db 71 LCFILCVPEQATYITLQWVFSLLCKAVHFLIHTMHASFTLAASVLDRLAIVPM 130
 QY 132 KQVSHNYTWSVLA--IWTVASLLPDPWFFSTIRIHGVEMLCVDPVAVAEPM 189
 Db 131 HSPFLP--TPNALAAIGLWGLLLESQPYLSYSSQSLANLTVCHPMSAPPRAMEL 188
 QY 189 ----FQVYPELLAFGLPIFASVYFPAVDQWFFPTKTONLPNCPSPQVTVMLLSIAI 244
 Db 189 QTFVFSYLLPVLIVISYARTIHLVPTVFPV-AAQSGSDPAV-----PFTVPMIVIVAV 242
 QY 245 ISALLKLPFWAKWWMHLYAAIPARTQFTALEVLMFESSAHLPLFVWSEFFEL 304
 Db 243 LFCQWNSHALLICVWFQGFELTPATYALFILSHVGVANSTVNFIVVALVSEHPFVF 302
 QY 305 KGVWFWMITTFPTVSE2--FTFANSEILPDPVFSERF--ASTFAPKFKVSSSSGK 360
 Db 303 PKICAGILPPAPPASPVCLAPNSHSGMLE---PESTLUTQVSEAGHLVPA-----354
 QY 361 KTEKAEIPLPD 372
 Db 355 -----PALPN 369

RESULT 2

US-09-828-432-3
 : Sequence 9, Application US/08933424B
 : Patent No. 6337206

GENERAL INFORMATION:

: APPLICANT: Tan, Carina
 : APPLICANT: Kollakowski, Lee F, Jr
 : TITLE OF INVENTION: METSE GALANIN RECEPTOR GALT2 AND
 : TITLE OF INVENTION: NUCLEOTIDE SEQUENCES
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Merck & Co., Inc
 : STREET: P.O. Box 2000, 126 E. Lincoln Ave.
 : CITY: Rahway
 : STATE: NJ
 : COUNTRY: USA
 : ZIP: 07065-0900

: COMPUTER READABLE FORM
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM compatible
 : OPERATING SYSTEM: Windows
 : SOFTWARE: FastSeq for Windows Version 2.0b
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/828-432-3
 : FILING DATE: 18-DEC-1997
 : CLASSIFICATION: 536
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/033,851
 : FILING DATE: 27-DEC-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Heber, Sheldon O.
 : REGISTRATION NUMBER: 14,170
 : REFERENCE/DOCKET NUMBER: 19846NF2
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 732-594-1958
 : TELEFAX: 732-594-4720
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 9
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 371 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: post-in

US-09-828-432-3

Query Match: 12.48; Score 269.5; DB 4; Length 414

Best Local Similarity: 24.78; Prod. No. 1.1e 147

Matches: 99; Conservative: 61; Mismatches: 178; Indels: 41; Gaps: 112

QY 12 GGYLPSSQWPTIFALLVAVCLVGFVGM/VIGIILLHNAWKGKPMIHSLLIISLAD 71
 Db 18 GSWPE-----AVLVPEFFALIFLVGAAGNAVLAVLEFG3---QAVSTTNLFIHLGVAD 70
 QY 72 LSLLESAPATAYSGVWGLWMPVYKSDWPIHTCMAAYSLTIIVVAVFVPMVSDPA 131
 Db 71 LCFILCVPEQATYITLQWVFSLLCKAVHFLIHTMHASFTLAASVLDRLAIVPM 130
 QY 132 KQVSHNYTWSVLA--IWTVASLLPDPWFFSTIRIHGVEMLCVDPVAVAEPM 189
 Db 131 HSPFLP--TPNALAAIGLWGLLLESQPYLSYSSQSLANLTVCHPMSAPPRAMEL 188
 QY 189 ----FQVYPELLAFGLPIFASVYFPAVDQWFFPTKTONLPNCPSPQVTVMLLSIAI 244
 Db 189 QTFVFSYLLPVLIVISYARTIHLVPTVFPV-AAQSGSDPAV-----PFTVPMIVIVAV 242
 QY 245 ISALLKLPFWAKWWMHLYAAIPARTQFTALEVLMFESSAHLPLFVWSEFFEL 304
 Db 243 LFCQWNSHALLICVWFQGFELTPATYALFILSHVGVANSTVNFIVVALVSEHPFVF 302
 QY 305 KGVWFWMITTFPTVSE2--FTFANSEILPDPVFSERF--ASTFAPKFKVSSSSGK 360
 Db 303 PKICAGILPPAPPASPVCLAPNSHSGMLE---PESTLUTQVSEAGHLVPA-----354
 QY 361 KTEKAEIPLPD 372
 Db 355 -----PALPN 369

RESULT 3

US-09-199-737-5

Sequence 5, Application US/09/199-737-5

Patent No. 6287788

GENERAL INFORMATION:

: APPLICANT: Bard, Jonathan A.
 : APPLICANT: Borowsky, Beth
 : APPLICANT: Smith, Kelli E.
 : APPLICANT: Brachek, Theresa A.
 : APPLICANT: Getald, Christophe P.G.
 : APPLICANT: Jones, Kenneth A.

: TITLE OF INVENTION: DNA Encoding GalP Receptor
 : FILE REFERENCE: 52241 C PCT US
 : CURRENT APPLICATION NUMBER: US/09/199-737-5
 : CURRENT FILING DATE: 1998-11-25
 : NUMBER OF SEQ ID NOS: 59
 : SOFTWARE: Patent In Ver. 2.0 beta
 : SEQ ID NO 5
 : LENGTH: 346
 : TYPE: PRT
 : ORGANISM: Rat
 : US-09-199-737-5

Query Match: 12.48; Score 269.5; DB 4; Length 414

Best Local Similarity: 27.18; Prod. No. 1.1e 147

Matches: 88; Conservative: 60; Mismatches: 110; Indels: 47; Gaps: 112

QY 36 GGFVJNLVIGIILLHNAWKGKPMIHSLLIISLAD 71
 Db 45 MGVLGSLVITVLAESK POFSTSTNLFIHLGAVLFIHTLAVALVSEHPFVF 130
 QY 95 WFTVSESWHTIINAAHLLIVTAVPDTAIPALNLT 147
 Db 104 AFICK...PIH...YPTVSMIVGIFTHAAMSDRYVAIVHSEKSHIEVFWALL 164
 QY 148 --IWTVASLLPDPWFFSTIRIHGVEMLCVDPVAVAEPM 189
 Db 155 VGFVJNLVIGIILLHNAWKGKPMIHSLLIISLAD 71

QY 200 I L P L P A S F W E P A V C G Y P P T T C N L Q C S K V T V M L S I A I S A L L W L P E W A M L W 269
DB 209 I P L L I C P Y A V I L H L H P L L A N S P Y S E A S Y K Y T A C T V I V V V V P O I S L P H V I H W 267
QY 260 V H L K A A P A P C G R I - A L S V L M F S I S S A N P L I F V M S E F F P E L G V W W M I T F Y P P 317
DB 269 A E F - G A P L T P A S F F R I T A C L A Y S S V N P I I A E L S E N F P K A V C V F E C V - - - - - 300
QY 318 T V S E S Q E T T A C S E G L S K V E S P E S 342
DB 321 - - C N E S P H C A K E K R I D T P S 340

RESULT 4
US-08-993-088A-3
; Sequence 3, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; TITLE OF INVENTION: GALANIN RECEPTOR GALP2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-993-088A-3

Query Match 12.4%, Score 269.5, DB 4, Length 346;
Best Local Similarity 27.1%, Pred. No. 1.5e-14;
Matches 99, Conservative 60, Mismatches 130, Indels 47, Gaps 15;

QY 36 V F V E N L V I G I L L H N A W K E P - S M I H S I L L S L A L L S L L P S A P I P A T A Y S V S W M L G 94
DB 45 M V L N S L A T I A F S K P G F T S T N L I L S L A L L S L A L L S L L P S A P I P A T A Y S V S W M L G 103
QY 95 M V F V S R W F I H T C W A A S L T I V W A V C F M A S R A Q V S T - H N Y T T S V I V A - - - - - 147
DB 104 A P I C K - F I H - - - Y F T S M L V S I T L A A M S V T R I V A V H S P R S S L F V S P N A L G 154
QY 148 - I W T A S L L I L P E F F S T I R H E V E - M C L V T V T A A E E M S E F Y L P L - L A P S - - - 199

DB 155 V S I M A L S I A M A S V A V Y - G L P H E D S L T E W E H W P - - - - - N O L U R E A V A V T P E R A M L 151
QY 200 I L P P A S F W E P A V C G Y P P T T C N L Q C S K V T V M L S I A I S A L L W L P E W A M L W 269
DB 209 I P L L I C P Y A V I L H L H P L L A N S P Y S E A S Y K Y T A C T V I V V V V P O I S L P H V I H W 267
QY 260 V H L K A A P A P C G R I - A L S V L M F S I S S A N P L I F V M S E F F P E L G V W W M I T F Y P P 317
DB 269 A E F - G A P L T P A S F F R I T A C L A Y S S V N P I I A E L S E N F P K A V C V F E C V - - - - - 300
QY 318 T V S E S Q E T T A C S E G L S K V E S P E S 342
DB 321 - - C N E S P H C A K E K R I D T P S 340

RESULT 5

US-08-993-424B-3
; Sequence 3, Application US/08993424B
; Patent No. 6337206
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Kolakowski, Lee P. Jr.
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALP2 AND
; TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,424B
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19846RP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-993-424B-3

Query Match 12.4%, Score 269.5, DB 4, Length 346;
Best Local Similarity 27.1%, Pred. No. 1.5e-14;
Matches 99, Conservative 60, Mismatches 130, Indels 47, Gaps 15;

QY 36 V F V E N L V I G I L L H N A W K E P - S M I H S I L L S L A L L S L L P S A P I P A T A Y S V S W M L G 94
DB 45 M V L N S L A T I A F S K P G F T S T N L I L S L A L L S L A L L S L L P S A P I P A T A Y S V S W M L G 103
QY 95 M V F V S R W F I H T C W A A S L T I V W A V C F M A S R A Q V S T - H N Y T T S V I V A - - - - - 147
DB 104 A P I C K - F I H - - - Y F T S M L V S I T L A A M S V T R I V A V H S P R S S L F V S P N A L G 154
QY 148 - I W T A S L L I L P E F F S T I R H E V E - M C L V T V T A A E E M S E F Y L P L - L A P S - - - 199

QY 148 ---INTVASLLPLPWFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 199
 DE 155 VGFWALGIAAGAVAYQQLFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 208
 QY 200 LPLPFAFSEVWPAYQQLFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 259
 DE 209 LPLPFAFSEVWPAYQQLFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 267
 QY 260 VWHKAAKAPAPGPTI--ALSOVMFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 317
 DE 268 AEF--GAPFLTASFFFTTAHCLAVNSMSSWDITVAFISENFFKAYKQVPCV..... 320
 QY 318 TVSESOETPAGNSEGLPKVPSPES 342
 DE 321 ----CNESPHGDAKE-KNRIDTPES 340

RESULT 6

US-09-058-333A-5
 ; Sequence 5, Application US/09058333A
 ; Patent No. 6144139
 ; GENERAL INFORMATION:
 ; APPLICANT: Bard, Jonathan A
 ; APPLICANT: Borowsky, Beth
 ; APPLICANT: Smith, Kelli E
 ; TITLE OF INVENTION: RNA ENCODING GALANIN GALS3 RECEPTORS
 ; TITLE OF INVENTION AND USE THEREOF
 ; NUMBER OF SEQUENCES: 65
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U S A
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1 0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/058,333A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P
 ; REGISTRATION NUMBER: 28,678
 ; PREFERENCE/AGENT NUMBER: 50741; F/CPW/EIP
 ; TELEPHONE: 212 378 0400
 ; TELEFAX: 212 301 0525
 ; INFORMATION FOR SEQ ID NO. 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-09-058-333A-5

Query Match 12.4%, Score 209.5, DB 4, Length 346,
 Best Local Similarity 27.1%, P-Val 1e-14,
 Matches 99; Conservative 60; Mismatches 130; Indels 47; Gaps 15;
 QY 36 VGFVWNLGCTGILLHAKWQFF-SMHSUHLNLSLCLSLLESADIPATAYFSWGLG 94
 DE 45 MGVLGNSIVITVARSF-PGPFSTTNLFNLSIACAYLFCIFQATVVALFTWVLG 103
 QY 95 WFFVFSSTWFIHMAAFSTIVVAVVPMVASTAPAVSYIRVTVIWEVLA..... 147
 DE 104 AFICK----FIH-----YFTVSWLSVIFTAAMSVPVVAIVHSPPSSSLPSPNALLG 154

QY 148 ---INTVASLLPLPWFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 199
 DE 155 VGFWALGIAAGAVAYQQLFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 208
 QY 200 LPLPFAFSEVWPAYQQLFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 259
 DE 209 LPLPFAFSEVWPAYQQLFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 267
 QY 260 VWHKAAKAPAPGPTI--ALSOVMFSTIRHGV MCLVDVPAVAEEMSMCKLYPL--LAFG-- 317
 DE 268 AEF--GAPFLTASFFFTTAHCLAVNSMSSWDITVAFISENFFKAYKQVPCV..... 320
 QY 318 TVSESOETPAGNSEGLPKVPSPES 342
 DE 321 ----CNESPHGDAKE-KNRIDTPES 340

RESULT 7

US-08-513-974B-46
 ; Sequence 46, Application US/08513974B
 ; Patent No. 6114139
 ; GENERAL INFORMATION:
 ; APPLICANT: Hiruma, Shuji
 ; APPLICANT: Hosoya, Masaki
 ; APPLICANT: Fujii, Ryo
 ; APPLICANT: Ohtaki, Tetsuya
 ; APPLICANT: Fukusumi, Shoji
 ; APPLICANT: Ohji, Kazuhiko
 ; TITLE OF INVENTION: 5 PROTEIN COILED PROTEIN RECEPTOR
 ; NUMBER OF SEQUENCES: 380
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GIFF, BRONSTEIN, ROBERTO & CUSHMAN, LLP
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent Release #1.0, Version #1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/513,974B
 ; FILING DATE: 14-SEP-1895
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-236357
 ; FILING DATE: 10-AUG-1895
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-093989
 ; FILING DATE: 19-AUG-1895
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7 057186
 ; FILING DATE: 16-MAR-1895
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 7-007177
 ; FILING DATE: 20-JAN-1895
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6 326611
 ; FILING DATE: 28-DEC-1894
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-270017
 ; FILING DATE: 02-NOV-1894
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6-236357
 ; FILING DATE: 30-SEP-1894
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6 236356
 ; FILING DATE: 30-SEP-1894
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 6 189274

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; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JF 6 190273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JF 6 190272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-46

```

```

Query Match 12.4%; Score 269; DB 3; Length 348;
Best Local Similarity 28.3%; Pred. No. 1.6e-14;
Matches 87; Conservative 54; Mismatches 128; Indels 38; Gaps 14;

QY 36 VGFVGNLGVIGILLHNWAKGKP-SMIHSLILNLSLADLSLLFSAPIPATAYSKSVNCLG 94
Db 46 MGV/LNSLIVITVLAPSK-PGKPPSTTNILFIILNLSIADLVLFLCIPQATVYALPTWVLG 104
QY 95 WFKVCKSSDMFZHTCMARKSLTIIVVAKVCFMYASDPAPQVGI-HNYTWSVLVA-----147
Db 105 AFICY----FIH-----VFETVSLVSIETLAAMSVDYVAIVHSRPSISLPVSPNALLG 155
QY 148 ---TWTVASLLPLPWFSTTPIHKGVE-MCLIVVPVAVAEPMMPGKLYPL--LAPG--199
Db 156 VGFVWALSIAMASPVAYVQPIPHRDSNTEFWGQWP-----NFIHPKAYVVMVTEFVSYL 209
QY 250 LPLFPAGVFPVAVGCTPPPTTYTQNFNQ:PSQVTVMLSTAIISALLWLFEMVAMW 259
Db 210 LFLLLTFTYAVLNHLHKF-IFMSKSESEASKFCTACTVUUVVVVFSKLPFHVVHLM 249
QY 260 VMLHPAA-PATPQGT-ALSCVLMFSLSSANPLIFLWSESEFEGPLGVWVWMTITFFP 317
Db 269 AEF--CAPLTTFASFFRITAHCLAYSSNVTILVAFSESEIFRPAVEVFFCHVULESH 324
QY 318 TVSESOE 324
Db 327 R-SETKE 332

```

```

RESULT 8
US-08-993-088A-10
; Sequence 10, Application US/08993088A
; Patent No. 6287855
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Sullivan, Kathleen
; TITLE OF INVENTION: GALANIN RECEPTOR GALK2 AND
; TITLE OF INVENTION: NOCTECTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P O Box 2000, 126 E Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows

```

```

; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,088A
; FILING DATE: 18-DEC-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/033,851
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 19946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1958
; TELEFAX: 732 594 4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-993-088A-10

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Query Match 12.4%; Score 269; DB 4; Length 348;
Best Local Similarity 29.3%; Pred. No. 1.6e-14;
Matches 87; Conservative 54; Mismatches 128; Indels 38; Gaps 14;

QY 36 VGFVGNLGVIGILLHNWAKGKP-SMIHSLILNLSLADLSLLFSAPIPATAYSKSVNCLG 94
Db 46 MGV/LNSLIVITVLAPSK-PGKPPSTTNILFIILNLSIADLVLFLCIPQATVYALPTWVLG 104
QY 95 WFKVCKSSDMFZHTCMARKSLTIIVVAKVCFMYASDPAPQVGI-HNYTWSVLVA-----147
Db 105 AFICY----FIH-----VFETVSLVSIETLAAMSVDYVAIVHSRPSISLPVSPNALLG 155
QY 148 IMTVASLLPLPWFSTTPIHKGVE-MCLIVVPVAVAEPMMPGKLYPL--LAPG--199
Db 156 VGFVWALSIAMASPVAYVQPIPHRDSNTEFWGQWP-----NFIHPKAYVVMVTEFVSYL 209
QY 250 LPLFPAGVFPVAVGCTPPPTTYTQNFNQ:PSQVTVMLSTAIISALLWLFEMVAMW 259
Db 210 LFLLLTFTYAVLNHLHKF-IFMSKSESEASKFCTACTVUUVVVVFSKLPFHVVHLM 249
QY 260 VMLHPAA-PATPQGT-ALSCVLMFSLSSANPLIFLWSESEFEGPLGVWVWMTITFFP 317
Db 269 AEF--CAPLTTFASFFRITAHCLAYSSNVTILVAFSESEIFRPAVEVFFCHVULESH 324
QY 318 TVSESOE 324
Db 327 R-SETKE 332

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RESULT 9
US-08-993-424B-10
; Sequence 10, Application US/08993424B
; Patent No. 6337206
; GENERAL INFORMATION:
; APPLICANT: Tan, Carina
; APPLICANT: Koliakowski, Lee F., Jr.
; TITLE OF INVENTION: MOUSE GALANIN RECEPTOR GALK2 AND
; TITLE OF INVENTION: NOCTECTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P O Box 2000, 126 E Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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? COMPUTER: IBM Compatible
? OPERATING SYSTEM: Windows
? SOFTWARE: FASTSEQ for Windows Version 2.0.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/98/933.424B
? FILING DATE: 18-DEC-1997
? CLASSIFICATION: 516
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 98/033.951
? FILING DATE: 27 DEC 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Hebel, Sheldon O.
? REGISTRATION NUMBER: 39,179
? REFERENCE/COCKET NUMBER: 1984CNP2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 732-594-1958
? TELEFAX: 732-594-4720
? TELEX:
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 346 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-993-424B-10

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Query March 12-48; Score 259; EP 4; Length 349;
Best local Similarity 28.38; Pred. No. 1.66 14;
Matches 87; Conservative 54; Mismatches 109; Indels 19; Gaps 14.

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QY 36 VGFVGNQVIGILLNNAWKKPK EMHUSLIMSTATGILLFSAIPATATSPSWWLG 94
Db 36 VGFVGNQVIGILLNNAWKKPK EMHUSLIMSTATGILLFSAIPATATSPSWWLG 94
QY 40 NQVLSLITVLAKE EHFESTLILHLSLALALILSIFFCATVAGLTWVLS 104
Db 40 NQVLSLITVLAKE EHFESTLILHLSLALALILSIFFCATVAGLTWVLS 104
QY 95 WPFYSGFPIHPTMAAPSLITVVAFTFMAVSDPAFTVSI-HRYTMSVLA 142
Db 95 WPFYSGFPIHPTMAAPSLITVVAFTFMAVSDPAFTVSI-HRYTMSVLA 142
QY 105 AFICK-----PIH-----YFTVGMVCIFFLAAMSTRTVAIVHSPFSSQIVCPNALG 156
Db 105 AFICK-----PIH-----YFTVGMVCIFFLAAMSTRTVAIVHSPFSSQIVCPNALG 156
QY 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSGKLYEL--LARG - 199
Db 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSGKLYEL--LARG - 199
QY 196 VRIKALSLANAGFVAHSLHSLHLSNQTQWEGW DELHFAVVTITVEGL 209
Db 196 VRIKALSLANAGFVAHSLHSLHLSNQTQWEGW DELHFAVVTITVEGL 209
QY 200 LPECHAFYHWEAYGCKEFGKRLHEDGIRSFVTVWMLTATLALALMFVWAMLM 210
Db 200 LPECHAFYHWEAYGCKEFGKRLHEDGIRSFVTVWMLTATLALALMFVWAMLM 210
QY 210 LPLLLCPYAKVLHLHF LFQMSPPFASPPFTALVLLVWVVFSSSLHVVHML 218
Db 210 LPLLLCPYAKVLHLHF LFQMSPPFASPPFTALVLLVWVVFSSSLHVVHML 218
QY 260 VMLKAAAGAPFPGFI ALSQVLMSSISANLILVNSFFPP GHWVWMMITTFPP 317
Db 260 VMLKAAAGAPFPGFI ALSQVLMSSISANLILVNSFFPP GHWVWMMITTFPP 317
QY 318 TVSESG 321
Db 318 TVSESG 321
QY 327 R-SETRE 332
Db 327 R-SETRE 332

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RESULT 10

US-08-540-9508-4

Sequence 2, Application US/085406508

Patent No. 639325

GENERAL INFORMATION:

APPLICANT: HINUMA, SHUJI

APPLICANT: FUJII, RYO

APPLICANT: FUKUSIMI, SHOJI

APPLICANT: OHTAKI, Tetsuya

APPLICANT: HOSoya, Masaki

APPLICANT: OGCI, Kazuhiko

APPLICANT: ONDA, Haruo

TITLE OF INVENTION: CALAMIN EFFECTIVE ESTERILIZATION AND THE THEREOF

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 WATER STREET

```

? CITY: BOSTON
? STATE: MA
? COUNTRY: US
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: 98/033.951
? FILING DATE: 11 OCT-1996
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 7-134412
? FILING DATE: 31-MAY-1995
? APPLICATION NUMBER: 6-126616
? FILING DATE: 28-DEC-1994
? APPLICATION NUMBER: 6-247599
? FILING DATE: 13-OCT-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: RESNICK, DAVID S.
? REGISTRATION NUMBER: 34,335
? REFERENCE/COCKET NUMBER: 45901
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-523-3400
? TELEFAX: 617-523-6440
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 148
? TYPE: Amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: Peptide
? US-08-540-9508-2

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Query March 12-48; Score 269; EP 4; Length 349;

Best local Similarity 28.38; Pred. No. 1.66 14;

Matches 87; Conservative 54; Mismatches 109; Indels 19; Gaps 14.

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QY 36 VGFVGNQVIGILLNNAWKKPK EMHUSLIMSTATGILLFSAIPATATSPSWWLG 94
Db 36 VGFVGNQVIGILLNNAWKKPK EMHUSLIMSTATGILLFSAIPATATSPSWWLG 94
QY 40 NQVLSLITVLAKE EHFESTLILHLSLALALILSIFFCATVAGLTWVLS 104
Db 40 NQVLSLITVLAKE EHFESTLILHLSLALALILSIFFCATVAGLTWVLS 104
QY 95 WPFYSGFPIHPTMAAPSLITVVAFTFMAVSDPAFTVSI-HRYTMSVLA 142
Db 95 WPFYSGFPIHPTMAAPSLITVVAFTFMAVSDPAFTVSI-HRYTMSVLA 142
QY 105 AFICK-----PIH-----YFTVGMVCIFFLAAMSTRTVAIVHSPFSSQIVCPNALG 156
Db 105 AFICK-----PIH-----YFTVGMVCIFFLAAMSTRTVAIVHSPFSSQIVCPNALG 156
QY 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSGKLYEL--LARG - 199
Db 148 ----INTVASLLPPEFFSTIRHGEVE-MCLVDVPAVAEEFMSGKLYEL--LARG - 199
QY 196 VRIKALSLANAGFVAHSLHSLHLSNQTQWEGW DELHFAVVTITVEGL 209
Db 196 VRIKALSLANAGFVAHSLHSLHLSNQTQWEGW DELHFAVVTITVEGL 209
QY 200 LPECHAFYHWEAYGCKEFGKRLHEDGIRSFVTVWMLTATLALALMFVWAMLM 210
Db 200 LPECHAFYHWEAYGCKEFGKRLHEDGIRSFVTVWMLTATLALALMFVWAMLM 210
QY 210 LPLLLCPYAKVLHLHF LFQMSPPFASPPFTALVLLVWVVFSSSLHVVHML 218
Db 210 LPLLLCPYAKVLHLHF LFQMSPPFASPPFTALVLLVWVVFSSSLHVVHML 218
QY 260 VMLKAAAGAPFPGFI ALSQVLMSSISANLILVNSFFPP GHWVWMMITTFPP 317
Db 260 VMLKAAAGAPFPGFI ALSQVLMSSISANLILVNSFFPP GHWVWMMITTFPP 317
QY 318 TVSESG 321
Db 318 TVSESG 321
QY 327 R-SETRE 332
Db 327 R-SETRE 332

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RESULT 11

US-08-513-974B-343

Sequence 4, Application US/08513974B

Patent No. 6114139

GENERAL INFORMATION:

APPLICANT: HINUMA, SHUJI

APPLICANT: HOSoya, Masaki

APPLICANT: FUJII, RYO

APPLICANT: Ohtaki, Tetsuya

1 APPLICANT: Fukusumi, Shoji
 2 APPLICANT: Choji, Kazuhiko
 3 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
 4 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
 5 NUMBER OF SEQUENCES: 380
 6 CORRESPONDENCE ADDRESS:
 7 ADDRESSEE: DIFE, RONSTEIN, ROBERTS & CUSHMAN, LLP
 8 STREET: 130 Water Street
 9 CITY: Boston
 10 STATE: MA
 11 COUNTRY: USA
 12 ZIP: 02109
 13 COMPUTER READABLE FORM:
 14 MEDIUM TYPE: floppy disk
 15 COMPUTER: IBM PC compatible
 16 OPERATING SYSTEM: PC-DOS/MS-DOS
 17 SOFTWARE: Patent Release #1.0, Version #1.30
 18 CURRENT APPLICATION DATA:
 19 APPLICATION NUMBER: US/08/513,974B
 20 FILING DATE: 14-SEP-1995
 21 CLASSIFICATION: 536
 22 PRIOR APPLICATION DATA:
 23 APPLICATION NUMBER: PCT/JP95/01599
 24 FILING DATE: 10-AUG-1995
 25 PRIOR APPLICATION DATA:
 26 APPLICATION NUMBER: JP 7-093989
 27 FILING DATE: 19-AUG-1995
 28 PRIOR APPLICATION DATA:
 29 APPLICATION NUMBER: JP 7-057186
 30 FILING DATE: 16-MAR-1995
 31 PRIOR APPLICATION DATA:
 32 APPLICATION NUMBER: JP 7-007177
 33 FILING DATE: 20-JAN-1995
 34 PRIOR APPLICATION DATA:
 35 APPLICATION NUMBER: JP 6-326611
 36 FILING DATE: 28-DEC-1994
 37 PRIOR APPLICATION DATA:
 38 APPLICATION NUMBER: JP 6-270017
 39 FILING DATE: 02 NOV 1994
 40 PRIOR APPLICATION DATA:
 41 APPLICATION NUMBER: JP 6-236357
 42 FILING DATE: 30-SEP-1994
 43 PRIOR APPLICATION DATA:
 44 APPLICATION NUMBER: JP 6-236356
 45 FILING DATE: 30-SEP-1994
 46 PRIOR APPLICATION DATA:
 47 APPLICATION NUMBER: JP 6-189274
 48 FILING DATE: 11-AUG-1994
 49 PRIOR APPLICATION DATA:
 50 APPLICATION NUMBER: JP 6-189273
 51 FILING DATE: 11-AUG-1994
 52 PRIOR APPLICATION DATA:
 53 APPLICATION NUMBER: JP 6-189272
 54 FILING DATE: 11-AUG-1994
 55 ATTORNEY/AGENT INFORMATION:
 56 NAME: Peshlky, David S.
 57 REGISTRATION NUMBER: 34,295
 58 REFERENCE/DOCKET NUMBER: 45753
 59 TELECOMMUNICATION INFORMATION:
 60 TELEPHONE: 617-523-3400
 61 TELEFAX: 617-523-6440
 62 INFORMATION FOR SEQ ID NO: 343:
 63 SEQUENCE CHARACTERISTICS:
 64 LENGTH: 349 amino acids
 65 TYPE: amino acid
 66 STRANDEDNESS:
 67 TOPOLOGY: linear
 68 MOLECULE TYPE: peptide
 69 US-08-513-974B-343

Query Match 12.4%; Score 269; DB 3; Length 349;
 Best Local Similarity 28.3%; Pred. No. 1.6e-14;
 Matches 87; Conservative 55; Mismatches 127; Indels 38; Gaps 14;

35 VAEVGMICGICGLLHNAAKSKF SMHSLIMLSLALSLLEFSAFIPATATKSTWNL 34
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 40 MGVLGSLVITVLASFY PGFPGSTTNLFLRLSLACLAYELCFIIFCTATVATLFWL 104
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 45 WFTVYSSAFHTTMAAFSLTIWVAVFEMVASTFAKQVSIHNYTMCVLA 147
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Query Match 12.4%; Score 268; DB 4; Length 372;
 Best Local Similarity 25.1%; Pred. No. 2.2e-14;
 Matches 93; Conservative 60; Mismatches 174; Indels 44; Gaps 11;

11 AGCVLSESEETWTETTFALLVAVCVYVPTVENCVLVSLILHNAAWREFANHLILNML 70



[illegible]

RESULT 2

US-09-766-693-2

Sequence 2, Application US/29766693

Parent No. 1520010016337A1

NOTICE OF THE

APPLICANT: ELSHOURBAGY, NABIL

APPLICANT: MICHAÏLOVICH, DAVID

; APPLICANT: SHABON, USMAN

APPLICANT: SHABAN, USMAN
TITLE OF INVENTION: MOLECULAR CLONING OF A GALANIN LIKE 7TM

TITLE OF INVENTION: RECEPTOR (AXOR40)

FILE OF INVENTION: RELIEF
FILE REFERENCE: GP-70649-C1

| | |
|----------------------------|---------------|
| FILE REFERENCE | GP-70849-1 |
| CURRENT APPLICATION NUMBER | 13/09/766 693 |

CURRENT FILING DATE: 2001-01-13

PRIOR APPLICATION NUMBER: IIS 09/417 170

: PRIOR APPLICATION NUMBER: 115-11
 : PRIOR FILING DATE: 1999-10-12

; PRIOR FILING DATE: 1999 10-12
 : PRIOR APPLICATION NUMBER: UK 9

;; PRIOR APPLICATION NUMBER: HK 9
: PRIOR FILING DATE: 1999-08-24

; PRIOR FILING DATE: 1999-08-24
 ; NUMBER OF SEQ ID NOS: 2

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; NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 2.0

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; SUBJWARE: FAS
: SEQ ID NO 2

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; SEQ ID NO 2
:      LENGTH: 419

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; LENGTH: 41
; TYPE: PPT

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; TYPE: PRT
; COUNTRY: HOME COUNTRY

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; CONSTANTIN. II.
110-00-766-692-2

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|-----------------------|----------------|-----------------|----------|------------|
| Query Match | 100.0% | Score 2167 | DB 10 | Length 419 |
| Best Local Similarity | 100.0% | Prod No 148-174 | | |
| Matches 406 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |

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|-----|----|---|-----|
| 1 | QY | MNVFAHLHAGGYLPDSQDPTIPALLVAVLVLRVGNLCVIGILLHNAGKPSMI | 60 |
| 14 | Db | MNVFAHLHAGGYLPDSQDPTIPALLVAVLVLRVGNLCVIGILLHNAGKPSMI | 73 |
| 61 | QY | HSLIINI:SLADLSLLPFSAPIATAYKSVMLQWFCVFKSDWEIHTCMAAKSLTIWVA | 120 |
| 74 | Db | HSLIINI:SLADLSLLPFSAPIATAYKSVMLQWFCVFKSDWIHTCMAAKSLTIWVA | 133 |
| 121 | QY | KVCWYASDPAKQVSHNTIINSVLVAIWVASLPLPEWFFSTIRHHEGVEMCLVDPA | 180 |
| 134 | Db | KVCWYASDPAKQVSHNTIINSVLVAIWVASLPLPEWFFSTIRHHEGVEMCLVDPA | 193 |
| 181 | QY | VAEFEMGFCKIYPLAFLPLFFAFKFEWPAVTCVYFZPTKTN:PNQIPRSQVWTML | 240 |

[illegible]

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RESULT 3
US-09-828-432-2
: Sequence 2, Application US/09028432
: Patent No. US20020137132A1
: GENERAL INFORMATION:
: APPLICANT: Vogeli, Gabriel
: APPLICANT: Lind, Peter
: APPLICANT: Sellitz, Torsten
: APPLICANT: Berthold, Malin
: TITLE OF INVENTION: No. US20020137132A1: G Protein Coupled Receptors
: FILE REFERENCE: 00145-US1
: CURRENT APPLICATION NUMBER: US/09/828,432
: CURRENT FILING DATE: 2001-04-06
: PRIOR APPLICATION NUMBER: CA/195,228
: PRIOR FILING DATE: 2000-04-06
: PRIOR APPLICATION NUMBER: 60/251,313
: PRIOR FILING DATE: 2000-12-05
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patent version 3.0
: SEQ ID NO 2
: LENGTH: 419
: TYPE: PPT
: ORGANISM: Homo sapiens
US-09-828-432-2

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Query Match      100.0% Score 2167 DP 107 E00P3.41%
Best local Similarity 100.0% Freq No. 2.40 176%
Matches 406; Conservative 0; Mismatches 0; Gaps 0

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| QY | 1 | MNVSPAHLLFAGGVLSDSQWETIIPALIVAVTVIVPVNLTIVVILHDAWFPIIMV | 40 |
| DB | 14 | MNVSPAHLLFAGGVLSDSQWETIIPALIVAVTVIVPVNLTIVVILHDAWFPIIMV | 34 |
| QY | 61 | HSLLINLSLADLSLLFSAPHATATAYKSVMLQWQVFPKSSDWLHLSWAAPQVAVVVA | 120 |
| DB | 74 | HSLLINLSLADLSLLFSAPHATATAYKSVMLQWQVFPKSSDWLHLSWAAPQVAVVVA | 124 |
| QY | 121 | KVCVMYASDAKQVSHNYILWVIVAVTVASLLPIIRHFLHSLQVQVWV | 176 |
| DB | 134 | KVCVMYASDAKQVSHNYITVSVIVAVTVASGLPIFWHTFIRHFLHSLQVWV | 170 |
| QY | 181 | VAEEMSMQVPIVETLAEVETFEAETFEAVV | 236 |
| DB | 194 | VAFRMSMQVPIVPIVLAFLPIPFASFVFNPAVQVFWPTVETVETV | 230 |
| QY | 241 | SIATISALLMLPEWIAWLWVHLKAAGTAPQGFIALSVLVMWSSDAKPIFVWV | 297 |
| DB | 254 | SIATISALLMLPEWIAWLWVHLKAAGTAPQGFIALSVLVMWSSDAKPIFVWV | 294 |
| QY | 301 | REGLGKGVWVWMTTKFPTVTSQETANSENPIKVVSPSSIAV | 357 |
| DB | 314 | REGLGKGVWVWMTTKFPTVTSQETANSENPIKVVSPSSIAV | 353 |
| QY | 361 | PTXAEIPILEDVEQEWHERDTPVSDNDPIPMHPTGPHQV | 400 |
| DB | 374 | KTXAEIPIIPDVEQEWHERDTPVSDNDPIPMHPTGPHQV | 410 |

RESULT 4

US-10-080-960-5

: Sequence 5, Application iis/10080960

; Publication No. US20020197695A1

; PUBLICATION NO. 0220
; GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Glucksmann, Maria

APPLICANT: MEYERS, RACHEL

APPLICANT: MEYERS, RACHEL
TITLE OF INVENTION: SYSTEMS AND METHODS FOR

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|
| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 | 46 | 47 | 48 | 49 | 50 | 51 | 52 | 53 | 54 | 55 | 56 | 57 | 58 | 59 | 60 | 61 | 62 | 63 | 64 | 65 | 66 | 67 | 68 | 69 | 70 | 71 | 72 | 73 | 74 | 75 | 76 | 77 | 78 | 79 | 80 | 81 | 82 | 83 | 84 | 85 | 86 | 87 | 88 | 89 | 90 | 91 | 92 | 93 | 94 | 95 | 96 | 97 | 98 | 99 | 100 |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|-----|

THE UNIVERSITY OF MICHIGAN LIBRARY

FILE REFERENCE: 34155 20044 .00
CURRENT APPLICATION NUMBER: 15716080 960

; CURRENT APPLICATION NUMBER: 167197080, 960
 ; CURRENT FILING DATE: 2001-10-19

: SUBMIT FILING DATE: 2001-10-19
 : PRICE APPLICATION NUMBER: US 60/243 040

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/ PRIOR FILING DATE 2000-10-20
/ PRIOR APPLICATION NUMBER: US 60/242,099
/ PRIOR FILING DATE 2000-10-20
/ PRIOR APPLICATION NUMBER: US 60/241,992
/ PRIOR FILING DATE 2000-10-20
/ PRIOR APPLICATION NUMBER: US 60/242,637
/ PRIOR FILING DATE 2000-10-20
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PASADOC for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH 461
/ TYPE ppt
/ ORGANISM: Homo sapiens
US-10-080-960-5

```

```

Query Match      94 98, Score 2065, 22 2, Length 461,
Best Local Similarity 100 0%; Pred. No. 8 7e-167;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNVSEAHLEHAGGVLPCSCDWEFTIIFALLVAVITVGVGNLVGIIILHNAWEKFSMI 49
Db      1 MNVSEAHLEHAGGVLPCSCDWEFTIIFALLVAVITVGVGNLVGIIILHNAWEKFSMI 49

QY      61 HSLIINLSLADLSLLSAPATAYSPKSWDI GMPVTKPSDWEIHTMAAFSTITVVVA 100
Db      61 HSLIINLSLADLSLLSAPATAYSPKSWDI GMPVTKPSDWEIHTMAAFSTITVVVA 100

QY      121 KVCPMYASDPAKQVSIHNYITWSVVAITVVASLLPFEWFFSTIRHHEGVEMCLVDVFA 180
Db      121 KVCPMYASDPAKQVSIHNYITWSVVAITVVASLLPFEWFFSTIRHHEGVEMCLVDVPA 180

QY      181 VAEFMSMGFLYLLAFGLLPFASFEVWEYAYDQCTYKTKTNLNQIPSKQVTWMLL 240
Db      181 VAEFMSMGFLYLLAFGLLPFASFEVWEYAYDQCTYKTKTNLNQIPSKQVTWMLL 240

QY      241 STAIISALLMLPEWVAVLWVHLKAAGPAPQGGTIALSQVLMFTISSANPLIFLWSEEP 300
Db      241 STAIISALLMLPEWVAVLWVHLKAAGPAPQGGTIALSQVLMFTISSANPLIFLWSEEP 300

QY      301 KEELPGYVWAKMIFPKPTVTSSTETPAKNSSELTKPVSESPASILKEKFFSSSSQKG 360
Db      301 KEELPGYVWAKMIFPKPTVTSSTETPAKNSSELTKPVSESPASILKEKFFSSSSQKG 360

QY      361 KTKAEIPLIDVQFQWHERDTPVSQ 387
Db      361 KTKAEIPLIDVQFQWHERDTPVSQ 387

```

```

1 RESULT 5
2
3 US 10-090-569-2
4
5 Application US100905692
6
7 Publication No. US20030008120A1
8
9 GENERAL INFORMATION
10
11 APPLICANT: HINUMA, Shuji
12
13 FUJII, Ryo
14
15 FUKUSUMI, Shoji
16
17 OHTAKI, Tetsuya
18
19 HOSOYA, Masaki
20
21 OHGI, Kazuhiro
22
23 ONDA, Haruo
24
25 TITLE OF INVENTION: GALANTIN RETENFER-PROTEIN, PRODUCTION AND USE THEREOF
26
27 NUMBER OF SEQUENCES: 17
28
29 CORRESPONDENCE ADDRESS:
30
31 ADDRESSEE: DIKE, BRONSTEIN, POBERTS & CUSHMAN
32
33 STREET: 130 WATER STREET
34
35 CITY: BOSTON
36
37 STATE: MA
38
39 COUNTRY: US
40
41 ZIP: 02109
42
43 COMPUTER READABLE FORM:
44
45 MEDIUM TYPE: Diskette
46
47 COMPUTER: IBM Compatible
48
49 OPERATING SYSTEM: DOS

```

```

SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: IS-10-090,569
FILING DATE: 04-Mar-1992
CLASSIFICATION: <Unknown>
PRICER APPLICATION DATA:
APPLICATION NUMBER: 13829/510,650
FILING DATE: 11-OCT-1995
APPLICATION NUMBER: 7 134412
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 6 325610
FILING DATE: 28 DEC-1994
APPLICATION NUMBER: 6 247599
FILING DATE: 13-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: FERNICE, DAVID S
PG-STEP NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
IS-10-090-569-2

```

```

Query Match      12.4%; Score 269; DB 9; Length 344;
Post Local Similarity 28.3%; Pred. No. 2.1e 10;
Matches 87; Conservative 54; Mismatches 128; Indels 12; gaps 148
QY 36 VGFVHLCVGLLHHNAWKCP-SMTHCIIHLGLADLLLEFCATIDATAYKQKNCI 154
DB 46 MGVLGSLVTVVAFPK-QPFFSTIRLILSLADLAVLFCFFQATVIALEFVW 114
QY 96 WPKVYSPDFEHTMAAPSLTIVVAWVPMVASDPAYQVSI-HNYTIVSVLVA 140
DB 105 AFICK---PIH-----YFPTVSLVSIITLAAMSVDPVVAVHSPRESSLRVSRNAL 136
QY 148 ---IWTVALLPPEWFFSTIRHGEVE-MCLVDVPAVAEEEMSMGKIYPL-LAF 130
DB 156 VSDIALSLAMASDPVAYHGLFHPESNQTFQEQWP-----NLIHRAVAVVTEFQ 120
QY 200 LPLPEASPEWNAIDACEGFTQNPFLIESFVTWVLSLQATLSN-LWDEWYWK 160
DB 210 LPLLLICFVAPVTHLHPFLPMSPESEAQFFYTAQVAVVYVTFGLWIDHNTDM 144
QY 260 VMHLFAASAFQSFEL-ALSLVMSLISLQMLPLVMSSEFFSELENKMWVLEKTP 112
DB 260 AEP-GAPVLTASPEFVIAH-LATNSQVDFIVAPLCRPPAPVPIKHHVTEH 106
QY 318 TVSEOE 124
DB 327 P-SETVE 112

```

```

RESULT 6
      : 00-569-5
      : Sequence 5, Application US/10090569
      : Publication No. US20030008129A1
      : GENERAL INFORMATION:
      : APPLICANT: HINUMA, Shuji
      : FUJII, Eyo
      : FUKUSUMI, Shoiji
      : CHIYAKI, Tetsuya
      : HOSOGAI, Masaki
      : OHBI, Kazuhito
      : ONDA, Haruo
      : TITLE OF INVENTION: GALANIN RECEPTOR PROTEIN, PROMOTION AND USE THEREOF
      : NUMBER OF SEQUENCES: 17

```

CORRESPONDENCE ADDRESS
ADDRESSEE TYPE: RECREATION, FORESTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: US

ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/090,569
FILING DATE: 04-Mar-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/540,650
FILING DATE: 11-OCT-1995
APPLICATION NUMBER: 7-134412
FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 6-328610
FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-247599
FILING DATE: 13-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: PERSIN, DAVID S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 459-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 149
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO. 5:
US-10 090-569-5

Query Match 12.1%; Score 262.5, Db 9, Length 349;
Best Local Similarity 26.8%, Pval No. 7 4e-15,
Matches 88; Conservative 61, Mismatches 124, Indels 59, Gaps 16,

QY 36 VGFVGNLVIGILLHNAWKCP-SMHSLLNLNLADLSLLLESAPIRATAYSKSVNDLG 94
Db 46 LGVIGNSLVITVLARK-PGRPESTNLNLFNLISLADLALYLCIPFQATVVALPTWVLG 104
QY 95 WFCVCKSDWPIHTCMAAKSLTIWVAVKCFMVASDPKQVSI-HNYTIWSVLVA----- 147
Db 105 AFICK-----FIH-----YFETVSMVLSIPTLAAMSDVPYVAIVHSPSSSLVSPNALLG 155
QY 148 ---INTVASLLPLPEWFFSTIRHGV-----EMCLVDVPVAEAEPMFMGKLYPL- 195
Db 156 VGTWALSTAMASE-----VATGHEHFHPPASNGTFTWELWPCPPH-----FAYVVV 203
QY 196 LAFI LLEFASVEWFAVQYFSTPTCTCLPFLIRFVTVWVLSIALISALLWLP 242
Db 204 TEVEGHLPLILICFYAVVNIHLHFY-IPNMFYKSEAFPTTACTVLVVVVVFGLSWLP 262
QY 263 EWVAVLWVWHLKACGAPDPCPT--ALSQVLMFSISASFLPLVMSEFFPEGLGVWFK 310
Db 263 HHIHIIWARP--GVFPLTPASFLPITAHCLAYSNSVNPIIYVLSNFPRKAYKQVFK 320
QY 311 MITYKPTTUSEQRTACSGFLPKVVPSPES 342
Db 321 HT FPDHLCDFPKES PDIPTPS 343

RESULT 7
US-09-903-196A-2
Sequence 2, Application US/09093196A

Publication No. US2002/0184657A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: CLONING/GENOTYPING INCREASED REPRODUCTIVE LIFE-SPAN
FILE REFERENCE: P-359
CURRENT APPLICATION NUMBER: US/09/903,306A
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: US 60/217,179
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/252,299
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/284,205
PRIOR FILING DATE: 2001-01-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 423
TYPE: PRT
ORGANISM: Mus musculus
US-09-903-196A-2

Query Match 10.0%; Score 295.5, Db 6, Length 474;
Best Local Similarity 24.5%, Pval No. 1 1e-14,
Matches 101; Conservative 60, Mismatches 144, Indels 59, Gaps 17,

QY 6 AHLHFADSYLISDSQW PTLIFALLVA VLVVGVNPLVWLLH 10
Db 39 ASSHEWANYTFSEWNEVJFPEVCAETDITVFAILLVAVVETVTVVWVWVWVWV 94
QY 51 NAWKGRKSMHS-----LILNLSLAKESLLFSAIPKAIAYSKVWLSWVWVWVWV 106
Db 24 N-----QPMHSATLIVVLAVAKNITLITFTILVAVQVLSK V WVVVAVVAVY 152
QY 107 TQMAAKSLTIWVAVKCFMVASDPKQVSI-HNYTIWSVLVA----- 147
Db 153 CSLHVSALTITAIAPVGRVIMHPKFPKIPKIPKIPKIPKIPKIPKIPKIPKIP 153
QY 163 STIRHGV EMCLVDVPVAEAEPMFMGKLYPL- 195
Db 211 PTRYSEDIVRSCLPFPPTAFGLFWYVHATFILLHFLFLLVAVVAVVAVVAVVAVV 209
QY 214 FPR-TTTPHPSFQVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 214
Db 271 TIGEVITEGLALSPKPTVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 271
QY 276 ALSCLVLP-----SSASNLIFLQMSHFFHFFHFFHFFHFFHFFHFFHFFHFFH 289
Db 321 HTNHALYFAPLWFMASQTCYNFTYCWNIHNPVRLKAL 321
QY 329 NSESLFPVVF SFGGLASHTFFPFI SFGGLASHTFFPFI 329
Db 370 QEDPLSPVSPFVAVTEKSHSPAPFPHHLLSSSLVWVWVWVWVWVWVWVWVWVWV 4.

RESULT 8

US-10-029-009-9
Sequence 3, Application US/09093196A-2
Patent No. US2002/016417A1
GENERAL INFORMATION:
APPLICANT: Felsch, Jason S.
APPLICANT: Amis, David Allen
APPLICANT: Kalghargi, Krishna
APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection Based Sequencing of Hybridoma Cell Lines
FILE REFERENCE: 11035173 US2
CURRENT APPLICATION NUMBER: US/10/629,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9

Db 145 NPTGFFPISQAYLGVILWVIAVLSTPLFLANSILENVFHHQHSKALEF-LADKVVCTE 203
 QY 184 EF-----MSMEGLYLLAFGLPFEASFYFWAYDQCKZKTKTONLRNOIPS---KOV 235
 Db 204 SWPLAHPHTIYITTELLIQYCTPLGFIILVCYAPIYPPQRCQVPHFQYTDLPAGHWQV 263
 QY 236 TWMLLSIAIISALLWPEWV AMLVWHLKAGAPAPQGFIALSQVLMFSISSANPLFLV 294
 Db 264 NVVLVGVYAPAVLMLPLHVSLESDWHEAIFICHGNIIFLVCHLLAMASTCWNFYIYG 323
 QY 295 VNCSEFPFGLKVVWVWVYVYPTTUSEQPTPAKNSGSP 334
 Db 324 PLNTNKKYKIFAL-----VLTCQOSAPLESEHLP 353

RESULT 13

US-09-292-973-19
 ; Sequence 19, Application US/0292973
 ; Patent No. US20020111473A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ZASTAWNY, Roman L.
 ; TITLE OF INVENTION: No. US20020111473A1:el G Protein Coupled Receptor
 ; FILE REFERENCE: 9074-9004
 ; CURRENT APPLICATION NUMBER: US/09/292-973
 ; PRIOR FILING DATE: 1998-04-16
 ; EARLIER APPLICATION NUMBER: US 60/081,995
 ; EARLIER FILING DATE: 1998-04-16
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 19
 ; LENGTH: 426
 ; TYPE: PRT
 ; ORGANISM: Rattus sp
 ; US-09-292-973-19

Query Match 9.5%; Score 205.5; DB 10; Length 426.

Best Local Similarity 24.5%; Pred. No. 6.7e-10;
 Matches 91; Conservative 54; Mismatches 170; Indels 57; Gaps 13;

QY 28 ALLVAVGVGVNLCVIGILLHNAWKQKPSMIHSLIINLSLADLSLLESAPIRATAYS 87
 Db 48 AAVVILFLCTVNTTVYFVLEK--FHMTVTNMFILHNAVCDLVGIFMFTLLVDNL 105
 QY 88 KSVMDLQWVCKSSDWFHTTMAAKSLTIIVVAVKVFVWVACDPAYQVSHNNTIMSVLVA 147
 Db 106 ITCMPEDNATCKMSGLVQMSVSASVFTLVAIVAEVFPGLVHPPEKLTLEKALFTIAV- 164
 QY 148 INTVASLLPLPEWFFSTI---RHHEGVEMCLVDVPAVAEEFMSEF-----KLYPLL 196
 Db 165 IVALALLMCPSSAVTLTVTFEEHH-----FMLDAPNPSYPLYSWGAWPEKMKRYTAV 213
 QY 197 AFG---LPLFEASFYFWFAVQCKKFG--TPTCNLSNQSVCQVTMLLSIAI 244
 Db 220 LPAHYIVPLALIVVMYVPIAPVLCQAPGAPDTEFAVAGPSTSPBPAPVVMIAWAL 279
 QY 245 ICAALLWLEFWAWLV---WHKKAAGAPATQGFIALSQVLMFSISSANPLFLV 295
 Db 280 PFTLSMLPLWVLLIDYGETSELQHLHLSVVAFP-----LAHMLAFPHSSANPLIYGY 322
 QY 296 MSEEPEEGKGVWV---KMTFFPTVSESETPAKNSGSPPTVPSPESP--ASIEPK 349
 Db 334 FNEHFFPGGCAAFACQVW-----PFWAAHVCAYSEPPNPLLPFPVVVVVQPSGLPSR 388
 QY 350 EKPSSSPSSGKGV 361
 Db 389 GPPSSGVPQPCR 400

RESULT 14

US-09-292-973-2
 ; Sequence 2, Application US/0292973
 ; Patent No. US20020111473A1

GENERAL INFORMATION:

; APPLICANT: ZASTAWNY, Roman L.
 ; APPLICANT: MCWHINNIE, Elizabeth A.
 ; TITLE OF INVENTION: No. US20020111473A1:el G Protein Coupled Receptor
 ; FILE REFERENCE: 9074-9004
 ; CURRENT APPLICATION NUMBER: US/09/292-973
 ; PRIOR FILING DATE: 1998-04-16
 ; EARLIER APPLICATION NUMBER: US 60/081,995
 ; EARLIER FILING DATE: 1998-04-16
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 432
 ; TYPE: PRT
 ; ORGANISM: Rattus sp.
 ; US-09-292-973-2

Query Match 9.5%; Score 205.5; DB 10; Length 432.

Best Local Similarity 24.5%; Pred. No. 6.7e-10;
 Matches 91; Conservative 54; Mismatches 170; Indels 57; Gaps 13;

QY 29 ALLVAVGVGVNLCVIGILLHNAWKQKPSMIHSLIINLSLADLSLLESAPIRATAYS 87
 Db 48 AAVVILFLCTVNTTVYFVLEK--FHMTVTNMFILHNAVCDLVGIFMFTLLVDNL 105
 QY 88 KSVMDLQWVCKSSDWFHTTMAAKSLTIIVVAVKVFVWVACDPAYQVSHNNTIMSVLVA 147
 Db 106 ITCMPEDNATCKMSGLVQMSVSASVFTLVAIVAEVFPGLVHPPEKLTLEKALFTIAV- 164
 QY 148 INTVASLLPLPEWFFSTI---RHHEGVEMCLVDVPAVAEEFMSEF-----KLYPLL 196
 Db 165 IVALALLMCPSSAVTLTVTFEEHH-----FMLDAPNPSYPLYSWGAWPEKMKRYTAV 213
 QY 197 AFG---LPLFEASFYFWFAVQCKKFG--TPTCNLSNQSVCQVTMLLSIAI 244
 Db 220 LPAHYIVPLALIVVMYVPIAPVLCQAPGAPDTEFAVAGPSTSPBPAPVVMIAWAL 279
 QY 245 ICAALLWLEFWAWLV---WHKKAAGAPATQGFIALSQVLMFSISSANPLFLV 295
 Db 280 PFTLSMLPLWVLLIDYGETSELQHLHLSVVAFP-----LAHMLAFPHSSANPLIYGY 322
 QY 296 MSEEPEEGKGVWV---KMTFFPTVSESETPAKNSGSPPTVPSPESP--ASIEPK 349
 Db 334 FNEHFFPGGCAAFACQVW-----PFWAAHVCAYSEPPNPLLPFPVVVVVQPSGLPSR 388
 QY 350 EKPSSSPSSGKGV 361
 Db 389 GPPSSGVPQPCR 400

RESULT 15

US-10-112-599A-2
 ; Sequence 2, Application US/10112599A
 ; Publication No. US2003010005476A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Keith D.
 ; TITLE OF INVENTION: ELISA-ASSAY FOR DETECTION OF INFECTION,
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING THERETO
 ; FILE REFERENCE: P-678
 ; CURRENT APPLICATION NUMBER: US/10/112,599A
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/290,513
 ; PRIOR FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PartSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-10-112-599A-2

Query Match 9.4%; Score 203.5; DB 9; Length 372;
 Best Local Similarity 23.8%; Pred. No. 9.1e-10;

